

SEQUENCE LISTING

<110> Jensen, Michael

<120> Selection Systems for Genetically
Modified Cells

<130> 24751-2502

<140> Unassigned

<141> Herewith

<160> 24

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1654

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (48)...(1589)

<223> Human Wild-type Inosine Monophosphate Dehydrogenase
II (IMPDH II)

<300>

<301> Collart, F.R. and Huberman, E.

<302> Cloning and sequence analysis of the human and

<303> J. Biol. Chem. (1988)

<304> 263

<306> 15769-15772

<400> 1

```

gaattcgggc ggtcctcgga gacacgcggc ggtgtcctgt gttggcc atg gcc gac      56
                                     Met Ala Asp
                                     1

tac ctg att agt ggg ggc acg tcc tac gtg cca gac gac gga ctc aca      104
Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp Gly Leu Thr
      5              10              15

gca cag cag ctc ttc aac tgc gga gac ggc ctc acc tac aat gac ttt      152
Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr Asn Asp Phe
      20              25              30              35

ctc att ctc cct ggg tac atc gac ttc act gca gac cag gtg gac ctg      200
Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln Val Asp Leu
      40              45              50

act tct gct ctg acc aag aaa atc act ctt aag acc cca ctg gtt tcc      248
Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro Leu Val Ser
      55              60              65

tct ccc atg gac aca gtc aca gag gct ggg atg gcc ata gca atg gcg      296
Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile Ala Met Ala
      70              75              80

ctt aca ggc ggt att ggc ttc atc cac cac aac tgt aca cct gaa ttc      344
Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr Pro Glu Phe
      85              90              95

```

cag gcc aat gaa gtt cgg aaa gtg aag aaa tat gaa cag gga ttc atc Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln Gly Phe Ile 100 105 110	392
aca gac cct gtg gtc ctc agc ccc aag gat cgc gtg cgg gat gtt ttt Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg Asp Val Phe 120 125 130	440
gag gcc aag gcc cgg cat ggt ttc tgc ggt atc cca atc aca gac aca Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile Thr Asp Thr 135 140 145	488
ggc cgg atg ggg agc cgc ttg gtg ggc atc atc tcc tcc agg gac att Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser Arg Asp Ile 150 155 160	536
gat ttt ctc aaa gag gag gaa cat gac tgt ttc ttg gaa gag ata atg Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu Glu Ile Met 165 170 175	584
aca aag agg gaa gac ttg gtg gta gcc ccc cgc agc atc aca ctg aag Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile Thr Leu Lys 180 185 190 195	632
gag gca aat gaa att ctg cag cgc agc aag aag gga aag ttg ccc att Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys Leu Pro Ile 200 205 210	680
gta aat gaa gat gat gag ctt gtg gcc atc att gcc cgg aca gac ctg Val Asn Glu Asp Glu Leu Val Ala Ile Ile Ala Arg Thr Asp Leu 215 220 225	728
aag aag aat cgg gac tac cca cta gcc tcc aaa gat gcc aag aaa cag Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala Lys Lys Gln 230 235 240	776
ctg ctg tgt ggg gca gcc att ggc act cat gag gat gac aag tat agg Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp Lys Tyr Arg 245 250 255	824
ctg gac ttg ctc gcc cag gct ggt gtg gat gta gtg gtt ttg gac tct Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val Leu Asp Ser 260 265 270 275	872
tcc cag gga aat tcc atc ttc cag atc aat atg atc aag tac atc aaa Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys Tyr Ile Lys 280 285 290	920
gac aaa tac cct aat ctc caa gtc att gga ggc aat gtg gtc act gct Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val Val Thr Ala 295 300 305	968
gcc cag gcc aag aac ctc att gat gca ggt gtg gat gcc ctg cgg gtg Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala Leu Arg Val 310 315 320	1016
ggc atg gga agt ggc tcc atc tgc att acg cag gaa gtg ctg gcc tgt Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu Ala Cys 325 330 335	1064
ggg cgg ccc caa gca aca gca gtg tac aag gtg tca gag tat gca cgg	1112

```

Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu Tyr Ala Arg
340                               345                               350                               355

cgc ttt ggt gtt ccg gtc att gct gat gga gga atc caa aat gtg ggt      1160
Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln Asn Val Gly
                               360                               365                               370

cat att gcg aaa gcc ttg gcc ctt ggg gcc tcc aca gtc atg atg ggc      1208
His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val Met Met Gly
                               375                               380                               385

tct ctc ctg gct gcc acc act gag gcc cct ggt gaa tac ttc ttt tcc      1256
Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr Phe Phe Ser
                               390                               395                               400

gat ggg atc cgg cta aag aaa tat cgc ggt atg ggt tct ctc gat gcc      1304
Asp Gly Ile Arg Leu Lys Tyr Tyr Arg Gly Met Gly Ser Leu Asp Ala
                               405                               410                               415

atg gac aag cac ctc agc agc cag aac aga tat ttc agt gaa gct gac      1352
Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser Glu Ala Asp
                               420                               425                               430                               435

aaa atc aaa gtg gcc cag gga gtg tct ggt gct gtg cag gac aaa ggg      1400
Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln Asp Lys Gly
                               440                               445                               450

tca atc cac aaa ttt gtc cct tac ctg att gct ggc atc caa cac tca      1448
Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile Gln His Ser
                               455                               460                               465

tgc cag gac att ggt gcc aag agc ttg acc caa gtc cga gcc atg atg      1496
Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala Met Met
                               470                               475                               480

tac tct ggg gag ctt aag ttt gag aag aga acg tcc tca gcc cag gtg      1544
Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala Gln Val
                               485                               490                               495

gaa ggt ggc gtc cat agc ctc cat tcg tat gag aag cgg ctt ttc      1589
Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu Phe
                               500                               505                               510

tgaaaaggga tccagcacac ctcctcggtt tttttttcaa taaaagttta gaaagacccg      1649
aattc                                                                1654

```

```

<210> 2
<211> 514
<212> PRT
<213> Homo sapien

```

```

<400> 2
Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
1      5      10
Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
20      25      30
Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
35      40      45
Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
50      55      60
Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
65      70      75      80

```

Ala	Met	Ala	Leu	Thr	Gly	Gly	Ile	Gly	Phe	Ile	His	His	Asn	Cys	Thr
				85					90					95	
Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Lys	Tyr	Glu	Gln
			100					105					110		
Gly	Phe	Ile	Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Lys	Asp	Arg	Val	Arg
		115					120					125			
Asp	Val	Phe	Glu	Ala	Lys	Ala	Arg	His	Gly	Phe	Cys	Gly	Ile	Pro	Ile
	130					135					140				
Thr	Asp	Thr	Gly	Arg	Met	Gly	Ser	Arg	Leu	Val	Gly	Ile	Ile	Ser	Ser
145					150					155					160
Arg	Asp	Ile	Asp	Phe	Leu	Lys	Glu	Glu	Glu	His	Asp	Cys	Phe	Leu	Glu
				165					170					175	
Glu	Ile	Met	Thr	Lys	Arg	Glu	Asp	Leu	Val	Val	Ala	Pro	Arg	Ser	Ile
			180					185					190		
Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys
		195					200					205			
Leu	Pro	Ile	Val	Asn	Glu	Asp	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg
	210					215					220				
Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ala
225					230					235					240
Lys	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	Asp	Asp
				245					250					255	
Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Ala	Gln	Ala	Gly	Val	Asp	Val	Val	Val
			260					265					270		
Leu	Asp	Ser	Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	Ile	Lys
		275					280					285			
Tyr	Ile	Lys	Asp	Lys	Tyr	Pro	Asn	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val
	290					295					300				
Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Ala
305					310					315					320
Leu	Arg	Val	Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val
				325					330					335	
Leu	Ala	Cys	Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	Ser	Glu
			340					345					350		
Tyr	Ala	Arg	Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Gln
		355					360					365			
Asn	Val	Gly	His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val
		370				375					380				
Met	Met	Gly	Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr
385					390					395					400
Phe	Phe	Ser	Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser
				405					410					415	
Leu	Asp	Ala	Met	Asp	Lys	His	Leu	Ser	Ser	Gln	Asn	Arg	Tyr	Phe	Ser
			420					425					430		
Glu	Ala	Asp	Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	Val	Gln
		435					440					445			
Asp	Lys	Gly	Ser	Ile	His	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Ala	Gly	Ile
	450					455					460				
Gln	His	Ser	Cys	Gln	Asp	Ile	Gly	Ala	Lys	Ser	Leu	Thr	Gln	Val	Arg
465					470					475					480
Ala	Met	Met	Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Ser	Ser
				485					490					495	
Ala	Gln	Val	Glu	Gly	Gly	Val	His	Ser	Leu	His	Ser	Tyr	Glu	Lys	Arg
			500					505					510		
Leu	Phe														

<210> 3
 <211> 1654
 <212> DNA
 <213> Homo sapien

```
<220>
<221> CDS
<222> (48)...(1589)
<223> T333I/S351Y Human IMPDH II mutant
```

```
<221> mutation
<222> 1045
<223> C to T mutation
```

```
<221> mutation
<222> 1046
<223> G to C mutation
```

```
<221> mutation
<222> 1099
<223> C to A mutation
```

```
<221> mutation
<222> 1100
<223> A to T mutation
```

<400> 3																
gaattcggggc ggtcctcggg gacacgcggc ggtgtcctgt gttggcc atg gcc gac																56
Met Ala Asp																
1																
tac ctg att agt ggg ggc acg tcc tac gtg cca gac gac gga ctc aca																104
Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp Gly Leu Thr																
5 10 15																
gca cag cag ctc ttc aac tgc gga gac ggc ctc acc tac aat gac ttt																152
Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr Asn Asp Phe																
20 25 30 35																
ctc att ctc cct ggg tac atc gac ttc act gca gac cag gtg gac ctg																200
Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln Val Asp Leu																
40 45 50																
act tct gct ctg acc aag aaa atc act ctt aag acc cca ctg gtt tcc																248
Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro Leu Val Ser																
55 60 65																
tct ccc atg gac aca gtc aca gag gct ggg atg gcc ata gca atg gcg																296
Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile Ala Met Ala																
70 75 80																
ctt aca ggc ggt att ggc ttc atc cac cac aac tgt aca cct gaa ttc																344
Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr Pro Glu Phe																
85 90 95																
cag gcc aat gaa gtt cgg aaa gtg aag aaa tat gaa cag gga ttc atc																392
Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln Gly Phe Ile																
100 105 110 115																
aca gac cct gtg gtc ctc agc ccc aag gat cgc gtg cgg gat gtt ttt																440
Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg Asp Val Phe																
120 125 130																
gag gcc aag gcc cgg cat ggt ttc tgc ggt atc cca atc aca gac aca																488
Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile Thr Asp Thr																
135 140 145																

ggc cgg atg ggg agc cgc ttg gtg ggc atc atc tcc tcc agg gac att	536
Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser Arg Asp Ile	
150 155 160	
gat ttt ctc aaa gag gag gaa cat gac tgt ttc ttg gaa gag ata atg	584
Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu Glu Ile Met	
165 170 175	
aca aag agg gaa gac ttg gtg gta gcc ccc cgc agc atc aca ctg aag	632
Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile Thr Leu Lys	
180 185 190 195	
gag gca aat gaa att ctg cag cgc agc aag aag gga aag ttg ccc att	680
Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys Leu Pro Ile	
200 205 210	
gta aat gaa gat gat gag ctt gtg gcc atc att gcc cgg aca gac ctg	728
Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg Thr Asp Leu	
215 220 225	
aag aag aat cgg gac tac cca cta gcc tcc aaa gat gcc aag aaa cag	776
Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala Lys Lys Gln	
230 235 240	
ctg ctg tgt ggg gca gcc att ggc act cat gag gat gac aag tat agg	824
Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Lys Tyr Arg	
245 250 255	
ctg gac ttg ctc gcc cag gct ggt gtg gat gta gtg gtt ttg gac tct	872
Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val Leu Asp Ser	
260 265 270 275	
tcc cag gga aat tcc atc ttc cag atc aat atg atc aag tac atc aaa	920
Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys Tyr Ile Lys	
280 285 290	
gac aaa tac cct aat ctc caa gtc att gga ggc aat gtg gtc act gct	968
Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val Val Thr Ala	
295 300 305	
gcc cag gcc aag aac ctc att gat gca ggt gtg gat gcc ctg cgg gtg	1016
Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala Leu Arg Val	
310 315 320	
ggc atg gga agt ggc tcc atc tgc att atc cag gaa gtg ctg gcc tgt	1064
Gly Met Gly Ser Gly Ser Ile Cys Ile Ile Gln Glu Val Leu Ala Cys	
325 330 335	
ggg cgg ccc caa gca aca gca gtg tac aag gtg tat gag tat gca cgg	1112
Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Tyr Glu Tyr Ala Arg	
340 345 350 355	
cgc ttt ggt gtt ccg gtc att gct gat gga gga atc caa aat gtg ggt	1160
Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln Asn Val Gly	
360 365 370	
cat att gcg aaa gcc ttg gcc ctt ggg gcc tcc aca gtc atg atg ggc	1208
His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val Met Met Gly	
375 380 385	
tct ctc ctg gct gcc acc act gag gcc cct ggt gaa tac ttc ttt tcc	1256
Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr Phe Phe Ser	

390					395					400						
gat	ggg	atc	cgg	cta	aag	aaa	tat	cgc	ggg	atg	ggg	tct	ctc	gat	gcc	1304
Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser	Leu	Asp	Ala	
	405					410					415					
atg	gac	aag	cac	ctc	agc	agc	cag	aac	aga	tat	ttc	agt	gaa	gct	gac	1352
Met	Asp	Lys	His	Leu	Ser	Ser	Gln	Asn	Arg	Tyr	Phe	Ser	Glu	Ala	Asp	
	420				425					430					435	
aaa	atc	aaa	gtg	gcc	cag	gga	gtg	tct	ggg	gct	gtg	cag	gac	aaa	ggg	1400
Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	Val	Gln	Asp	Lys	Gly	
			440						445					450		
tca	atc	cac	aaa	ttt	gtc	cct	tac	ctg	att	gct	ggc	atc	caa	cac	tca	1448
Ser	Ile	His	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Ala	Gly	Ile	Gln	His	Ser	
			455					460					465			
tgc	cag	gac	att	ggg	gcc	aag	agc	ttg	acc	caa	gtc	cga	gcc	atg	atg	1496
Cys	Gln	Asp	Ile	Gly	Ala	Lys	Ser	Leu	Thr	Gln	Val	Arg	Ala	Met	Met	
		470					475					480				
tac	tct	ggg	gag	ctt	aag	ttt	gag	aag	aga	acg	tcc	tca	gcc	cag	gtg	1544
Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Ser	Ser	Ala	Gln	Val	
	485					490					495					
gaa	ggg	ggc	gtc	cat	agc	ctc	cat	tcg	tat	gag	aag	cgg	ctt	ttc		1589
Glu	Gly	Gly	Val	His	Ser	Leu	His	Ser	Tyr	Glu	Lys	Arg	Leu	Phe		
	500				505				510							
tgaaaaggga	tccagcacac	ctcctcgggt	tttttttcaa	taaaagttta	gaaagaccg											1649
aattc																1654

<210> 4
 <211> 514
 <212> PRT
 <213> Homo sapien

<400> 4
 Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
 1 5 10 15
 Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
 20 25 30
 Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
 35 40 45
 Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
 50 55 60
 Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
 65 70 75 80
 Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
 85 90 95
 Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln
 100 105 110
 Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg
 115 120 125
 Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile
 130 135 140
 Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser
 145 150 155 160
 Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu
 165 170 175
 Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile

			180					185					190				
Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys		
		195					200					205					
Leu	Pro	Ile	Val	Asn	Glu	Asp	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg		
	210					215					220						
Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ala		
225					230					235					240		
Lys	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	Asp	Asp		
			245						250					255			
Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Ala	Gln	Ala	Gly	Val	Asp	Val	Val	Val		
		260					265						270				
Leu	Asp	Ser	Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	Ile	Lys		
	275					280						285					
Tyr	Ile	Lys	Asp	Lys	Tyr	Pro	Asn	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val		
	290					295					300						
Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Ala		
305				310						315					320		
Leu	Arg	Val	Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Ile	Gln	Glu	Val		
			325					330						335			
Leu	Ala	Cys	Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	Tyr	Glu		
		340						345					350				
Tyr	Ala	Arg	Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Gln		
	355						360					365					
Asn	Val	Gly	His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val		
	370					375					380						
Met	Met	Gly	Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr		
385				390						395					400		
Phe	Phe	Ser	Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser		
			405					410					415				
Leu	Asp	Ala	Met	Asp	Lys	His	Leu	Ser	Gln	Asn	Arg	Tyr	Phe	Ser			
		420						425					430				
Glu	Ala	Asp	Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	Val	Gln		
		435					440					445					
Asp	Lys	Gly	Ser	Ile	His	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Ala	Gly	Ile		
	450					455					460						
Gln	His	Ser	Cys	Gln	Asp	Ile	Gly	Ala	Lys	Ser	Leu	Thr	Gln	Val	Arg		
465				470						475					480		
Ala	Met	Met	Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Ser	Ser		
			485					490						495			
Ala	Gln	Val	Glu	Gly	Gly	Val	His	Ser	Leu	His	Ser	Tyr	Glu	Lys	Arg		
		500						505					510				

Leu Phe

<210> 5
 <211> 1654
 <212> DNA
 <213> Homo sapien

<220>
 <221> mutation
 <222> 877
 <223> A to G mutation

<221> CDS
 <222> (48)...(1589)
 <223> Gln277Arg Human IMPDH II mutant

<300>
 <301> Farazi et al.
 <303> J. Biol. Chem. (1997)
 <304> 271

<305> 2

<306> 961-965

<400> 5

```

gaattcgggc ggtcctcgga gacacgcggc ggtgtcctgt gttggcc atg gcc gac      56
                               Met Ala Asp
                               1

tac ctg att agt ggg ggc acg tcc tac gtg cca gac gac gga ctc aca      104
Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp Gly Leu Thr
      5                               10                               15

gca cag cag ctc ttc aac tgc gga gac ggc ctc acc tac aat gac ttt      152
Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr Asn Asp Phe
      20                               25                               30                               35

ctc att ctc cct ggg tac atc gac ttc act gca gac cag gtg gac ctg      200
Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln Val Asp Leu
                               40                               45                               50

act tct gct ctg acc aag aaa atc act ctt aag acc cca ctg gtt tcc      248
Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro Leu Val Ser
                               55                               60                               65

tct ccc atg gac aca gtc aca gag gct ggg atg gcc ata gca atg gcg      296
Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile Ala Met Ala
                               70                               75                               80

ctt aca ggc ggt att ggc ttc atc cac cac aac tgt aca cct gaa ttc      344
Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr Pro Glu Phe
      85                               90                               95

cag gcc aat gaa gtt cgg aaa gtg aag aaa tat gaa cag gga ttc atc      392
Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln Gly Phe Ile
      100                               105                               110                               115

aca gac cct gtg gtc ctc agc ccc aag gat cgc gtg cgg gat gtt ttt      440
Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg Asp Val Phe
                               120                               125                               130

gag gcc aag gcc cgg cat ggt ttc tgc ggt atc cca atc aca gac aca      488
Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile Thr Asp Thr
                               135                               140                               145

ggc cgg atg ggg agc cgc ttg gtg ggc atc atc tcc tcc agg gac att      536
Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser Arg Asp Ile
                               150                               155                               160

gat ttt ctc aaa gag gag gaa cat gac tgt ttc ttg gaa gag ata atg      584
Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu Glu Ile Met
      165                               170                               175

aca aag agg gaa gac ttg gtg gta gcc ccc cgc agc atc aca ctg aag      632
Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile Thr Leu Lys
      180                               185                               190                               195

gag gca aat gaa att ctg cag cgc agc aag aag gga aag ttg ccc att      680
Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys Leu Pro Ile
                               200                               205                               210

gta aat gaa gat gat gag ctt gtg gcc atc att gcc cgg aca gac ctg      728
Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg Thr Asp Leu

```

215					220					225						
aag	aag	aat	cgg	gac	tac	cca	cta	gcc	tcc	aaa	gat	gcc	aag	aaa	cag	776
Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ala	Lys	Lys	Gln	
		230					235					240				
ctg	ctg	tgt	ggg	gca	gcc	att	ggc	act	cat	gag	gat	gac	aag	tat	agg	824
Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	Asp	Asp	Lys	Tyr	Arg	
	245					250					255					
ctg	gac	ttg	ctc	gcc	cag	gct	ggg	gtg	gat	gta	gtg	gtt	ttg	gac	tct	872
Leu	Asp	Leu	Leu	Ala	Gln	Ala	Gly	Val	Asp	Val	Val	Val	Leu	Asp	Ser	
260				265				270							275	
tcc	cgg	gga	aat	tcc	atc	ttc	cag	atc	aat	atg	atc	aag	tac	atc	aaa	920
Ser	Arg	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	Ile	Lys	Tyr	Ile	Lys	
			280						285					290		
gac	aaa	tac	cct	aat	ctc	caa	gtc	att	gga	ggc	aat	gtg	gtc	act	gct	968
Asp	Lys	Tyr	Pro	Asn	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val	Val	Thr	Ala	
			295					300					305			
gcc	cag	gcc	aag	aac	ctc	att	gat	gca	ggg	gtg	gat	gcc	ctg	cgg	gtg	1016
Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Ala	Leu	Arg	Val	
		310					315					320				
ggc	atg	gga	agt	ggc	tcc	atc	tgc	att	acg	cag	gaa	gtg	ctg	gcc	tgt	1064
Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val	Leu	Ala	Cys	
	325					330					335					
ggg	cgg	ccc	caa	gca	aca	gca	gtg	tac	aag	gtg	tca	gag	tat	gca	cgg	1112
Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	Ser	Glu	Tyr	Ala	Arg	
340					345					350					355	
cgc	ttt	ggg	gtt	ccg	gtc	att	gct	gat	gga	gga	atc	caa	aat	gtg	ggg	1160
Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Gln	Asn	Val	Gly	
				360					365					370		
cat	att	gcg	aaa	gcc	ttg	gcc	ctt	ggg	gcc	tcc	aca	gtc	atg	atg	ggc	1208
His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val	Met	Met	Gly	
			375					380					385			
tct	ctc	ctg	gct	gcc	acc	act	gag	gcc	cct	ggg	gaa	tac	ttc	ttt	tcc	1256
Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr	Phe	Phe	Ser	
		390					395					400				
gat	ggg	atc	cgg	cta	aag	aaa	tat	cgc	ggg	atg	ggg	tct	ctc	gat	gcc	1304
Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser	Leu	Asp	Ala	
	405					410					415					
atg	gac	aag	cac	ctc	agc	agc	cag	aac	aga	tat	ttc	agt	gaa	gct	gac	1352
Met	Asp	Lys	His	Leu	Ser	Ser	Gln	Asn	Arg	Tyr	Phe	Ser	Glu	Ala	Asp	
420					425				430						435	
aaa	atc	aaa	gtg	gcc	cag	gga	gtg	tct	ggg	gct	gtg	cag	gac	aaa	ggg	1400
Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	Val	Gln	Asp	Lys	Gly	
				440					445					450		
tca	atc	cac	aaa	ttt	gtc	cct	tac	ctg	att	gct	ggc	atc	caa	cac	tca	1448
Ser	Ile	His	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Ala	Gly	Ile	Gln	His	Ser	
			455					460					465			

tgc cag gac att ggt gcc aag agc ttg acc caa gtc cga gcc atg atg 1496
 Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala Met Met
 470 475 480

tac tct ggg gag ctt aag ttt gag aag aga acg tcc tca gcc cag gtg 1544
 Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala Gln Val
 485 490 495

gaa ggt ggc gtc cat agc ctc cat tcg tat gag aag cgg ctt ttc 1589
 Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu Phe
 500 505 510

tgaaaaggga tccagcacac ctctcgggt tttttttcaa taaaagtta gaaagacccg 1649
 aattc 1654

<210> 6
 <211> 514
 <212> PRT
 <213> Homo sapien

<400> 6
 Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
 1 5 10 15
 Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
 20 25 30
 Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
 35 40 45
 Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
 50 55 60
 Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
 65 70 75 80
 Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
 85 90 95
 Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln
 100 105 110
 Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg
 115 120 125
 Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile
 130 135 140
 Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser
 145 150 155 160
 Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu
 165 170 175
 Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile
 180 185 190
 Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
 195 200 205
 Leu Pro Ile Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg
 210 215 220
 Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala
 225 230 235 240
 Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp
 245 250 255
 Lys Tyr Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val
 260 265 270
 Leu Asp Ser Ser Arg Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys
 275 280 285
 Tyr Ile Lys Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val
 290 295 300
 Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala
 305 310 315 320
 Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val

325 330 335
 Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu
 340 345 350
 Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln
 355 360 365
 Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
 370 375 380
 Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
 385 390 395 400
 Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
 405 410 415
 Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser
 420 425 430
 Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln
 435 440 445
 Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile
 450 455 460
 Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg
 465 470 475 480
 Ala Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser
 485 490 495
 Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg
 500 505 510
 Leu Phe

<210> 7
 <211> 1654
 <212> DNA
 <213> Homo sapien

<220>
 <221> mutation
 <222> 1431
 <223> G to A mutation

<221> CDS
 <222> (48)...(1589)
 <223> Ala462Thr Human IMPDH II mutant

<300>
 <301> Farazi et al.
 <303> J. Biol. Chem. (1997)
 <304> 272
 <305> 2
 <306> 961-965

<400> 7
 gaattcgggc ggtcctcgga gacacgcggc ggtgtcctgt gttggcc atg gcc gac 56
 Met Ala Asp
 1
 tac ctg att agt ggg ggc acg tcc tac gtg cca gac gac gga ctc aca 104
 Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp Gly Leu Thr
 5 10 15
 gca cag cag ctc ttc aac tgc gga gac ggc ctc acc tac aat gac ttt 152
 Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr Asn Asp Phe
 20 25 30 35
 ctc att ctc cct ggg tac atc gac ttc act gca gac cag gtg gac ctg 200
 Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln Val Asp Leu

40										45					50					
act	tct	gct	ctg	acc	aag	aaa	atc	act	ctt	aag	acc	cca	ctg	gtt	tcc	248				
Thr	Ser	Ala	Leu	Thr	Lys	Lys	Ile	Thr	Leu	Lys	Thr	Pro	Leu	Val	Ser					
			55					60					65							
tct	ccc	atg	gac	aca	gtc	aca	gag	gct	ggg	atg	gcc	ata	gca	atg	gcg	296				
Ser	Pro	Met	Asp	Thr	Val	Thr	Glu	Ala	Gly	Met	Ala	Ile	Ala	Met	Ala					
		70					75					80								
ctt	aca	ggc	ggg	att	ggc	ttc	atc	cac	cac	aac	tgt	aca	cct	gaa	ttc	344				
Leu	Thr	Gly	Gly	Ile	Gly	Phe	Ile	His	His	Asn	Cys	Thr	Pro	Glu	Phe					
	85					90				95										
cag	gcc	aat	gaa	gtt	cgg	aaa	gtg	aag	aaa	tat	gaa	cag	gga	ttc	atc	392				
Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Lys	Tyr	Glu	Gln	Gly	Phe	Ile					
100					105				110						115					
aca	gac	cct	gtg	gtc	ctc	agc	ccc	aag	gat	cgc	gtg	cgg	gat	gtt	ttt	440				
Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Lys	Asp	Arg	Val	Arg	Asp	Val	Phe					
				120					125					130						
gag	gcc	aag	gcc	cgg	cat	ggg	ttc	tgc	ggg	atc	cca	atc	aca	gac	aca	488				
Glu	Ala	Lys	Ala	Arg	His	Gly	Phe	Cys	Gly	Ile	Pro	Ile	Thr	Asp	Thr					
			135					140					145							
ggc	cgg	atg	ggg	agc	cgc	ttg	gtg	ggc	atc	atc	tcc	tcc	agg	gac	att	536				
Gly	Arg	Met	Gly	Ser	Arg	Leu	Val	Gly	Ile	Ile	Ser	Ser	Arg	Asp	Ile					
		150					155					160								
gat	ttt	ctc	aaa	gag	gag	gaa	cat	gac	tgt	ttc	ttg	gaa	gag	ata	atg	584				
Asp	Phe	Leu	Lys	Glu	Glu	Glu	His	Asp	Cys	Phe	Leu	Glu	Glu	Ile	Met					
	165					170					175									
aca	aag	agg	gaa	gac	ttg	gtg	gta	gcc	ccc	cgc	agc	atc	aca	ctg	aag	632				
Thr	Lys	Arg	Glu	Asp	Leu	Val	Val	Ala	Pro	Arg	Ser	Ile	Thr	Leu	Lys					
180					185				190						195					
gag	gca	aat	gaa	att	ctg	cag	cgc	agc	aag	aag	gga	aag	ttg	ccc	att	680				
Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys	Leu	Pro	Ile					
				200					205					210						
gta	aat	gaa	gat	gat	gag	ctt	gtg	gcc	atc	att	gcc	cgg	aca	gac	ctg	728				
Val	Asn	Glu	Asp	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg	Thr	Asp	Leu					
			215				220						225							
aag	aag	aat	cgg	gac	tac	cca	cta	gcc	tcc	aaa	gat	gcc	aag	aaa	cag	776				
Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ala	Lys	Lys	Gln					
		230					235					240								
ctg	ctg	tgt	ggg	gca	gcc	att	ggc	act	cat	gag	gat	gac	aag	tat	agg	824				
Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	Asp	Asp	Lys	Tyr	Arg					
	245					250					255									
ctg	gac	ttg	ctc	gcc	cag	gct	ggg	gtg	gat	gta	gtg	gtt	ttg	gac	tct	872				
Leu	Asp	Leu	Leu	Ala	Gln	Ala	Gly	Val	Asp	Val	Val	Val	Leu	Asp	Ser					
260					265				270						275					
tcc	cag	gga	aat	tcc	atc	ttc	cag	atc	aat	atg	atc	aag	tac	atc	aaa	920				
Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	Ile	Lys	Tyr	Ile	Lys					
				280					285					290						

gac aaa tac cct aat ctc caa gtc att gga ggc aat gtg gtc act gct	968
Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val Val Thr Ala	
295 300 305	
gcc cag gcc aag aac ctc att gat gca ggt gtg gat gcc ctg cgg gtg	1016
Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala Leu Arg Val	
310 315 320	
ggc atg gga agt ggc tcc atc tgc att acg cag gaa gtg ctg gcc tgt	1064
Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu Ala Cys	
325 330 335	
ggg cgg ccc caa gca aca gca gtg tac aag gtg tca gag tat gca cgg	1112
Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu Tyr Ala Arg	
340 345 350 355	
cgc ttt ggt gtt ccg gtc att gct gat gga gga atc caa aat gtg ggt	1160
Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln Asn Val Gly	
360 365 370	
cat att gcg aaa gcc ttg gcc ctt ggg gcc tcc aca gtc atg atg ggc	1208
His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val Met Met Gly	
375 380 385	
tct ctc ctg gct gcc acc act gag gcc cct ggt gaa tac ttc ttt tcc	1256
Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr Phe Phe Ser	
390 395 400	
gat ggg atc cgg cta aag aaa tat cgc ggt atg ggt tct ctc gat gcc	1304
Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser Leu Asp Ala	
405 410 415	
atg gac aag cac ctc agc agc cag aac aga tat ttc agt gaa gct gac	1352
Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser Glu Ala Asp	
420 425 430 435	
aaa atc aaa gtg gcc cag gga gtg tct ggt gct gtg cag gac aaa ggg	1400
Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln Asp Lys Gly	
440 445 450	
tca atc cac aaa ttt gtc cct tac ctg att act ggc atc caa cac tca	1448
Ser Ile His Lys Phe Val Pro Tyr Leu Ile Thr Gly Ile Gln His Ser	
455 460 465	
tgc cag gac att ggt gcc aag agc ttg acc caa gtc cga gcc atg atg	1496
Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala Met Met	
470 475 480	
tac tct ggg gag ctt aag ttt gag aag aga acg tcc tca gcc cag gtg	1544
Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala Gln Val	
485 490 495	
gaa ggt ggc gtc cat agc ctc cat tcg tat gag aag cgg ctt ttc	1589
Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu Phe	
500 505 510	
tgaaaaggga tccagcacac ctccctcggtt tttttttcaa taaaagttta gaaagaccg	1649
aattc	1654
<210> 8	
<211> 514	
<212> PRT	

<213> Homo sapien

<400> 8

Met	Ala	Asp	Tyr	Leu	Ile	Ser	Gly	Gly	Thr	Ser	Tyr	Val	Pro	Asp	Asp
1				5					10					15	
Gly	Leu	Thr	Ala	Gln	Gln	Leu	Phe	Asn	Cys	Gly	Asp	Gly	Leu	Thr	Tyr
			20					25					30		
Asn	Asp	Phe	Leu	Ile	Leu	Pro	Gly	Tyr	Ile	Asp	Phe	Thr	Ala	Asp	Gln
		35					40					45			
Val	Asp	Leu	Thr	Ser	Ala	Leu	Thr	Lys	Lys	Ile	Thr	Leu	Lys	Thr	Pro
	50					55					60				
Leu	Val	Ser	Ser	Pro	Met	Asp	Thr	Val	Thr	Glu	Ala	Gly	Met	Ala	Ile
65					70					75					80
Ala	Met	Ala	Leu	Thr	Gly	Gly	Ile	Gly	Phe	Ile	His	His	Asn	Cys	Thr
				85					90					95	
Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Lys	Tyr	Glu	Gln
			100					105					110		
Gly	Phe	Ile	Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Lys	Asp	Arg	Val	Arg
		115					120					125			
Asp	Val	Phe	Glu	Ala	Lys	Ala	Arg	His	Gly	Phe	Cys	Gly	Ile	Pro	Ile
	130					135					140				
Thr	Asp	Thr	Gly	Arg	Met	Gly	Ser	Arg	Leu	Val	Gly	Ile	Ile	Ser	Ser
145					150					155					160
Arg	Asp	Ile	Asp	Phe	Leu	Lys	Glu	Glu	Glu	His	Asp	Cys	Phe	Leu	Glu
				165				170						175	
Glu	Ile	Met	Thr	Lys	Arg	Glu	Asp	Leu	Val	Val	Ala	Pro	Arg	Ser	Ile
			180					185					190		
Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys
		195					200					205			
Leu	Pro	Ile	Val	Asn	Glu	Asp	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg
	210					215					220				
Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ala
225					230					235					240
Lys	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	Asp	Asp
				245					250					255	
Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Ala	Gln	Ala	Gly	Val	Asp	Val	Val	Val
			260					265					270		
Leu	Asp	Ser	Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	Ile	Lys
		275					280					285			
Tyr	Ile	Lys	Asp	Lys	Tyr	Pro	Asn	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val
	290					295					300				
Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Ala
305					310					315					320
Leu	Arg	Val	Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val
				325					330					335	
Leu	Ala	Cys	Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	Ser	Glu
			340					345					350		
Tyr	Ala	Arg	Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Gln
		355					360					365			
Asn	Val	Gly	His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val
	370					375					380				
Met	Met	Gly	Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr
385					390					395					400
Phe	Phe	Ser	Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser
				405					410					415	
Leu	Asp	Ala	Met	Asp	Lys	His	Leu	Ser	Ser	Gln	Asn	Arg	Tyr	Phe	Ser
			420					425					430		
Glu	Ala	Asp	Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	Val	Gln
		435					440					445			
Asp	Lys	Gly	Ser	Ile	His	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Thr	Gly	Ile
	450					455					460				
Gln	His	Ser	Cys	Gln	Asp	Ile	Gly	Ala	Lys	Ser	Leu	Thr	Gln	Val	Arg

```

465          470          475          480
Ala Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser
          485          490          495
Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg
          500          505          510
Leu Phe

```

```

<210> 9
<211> 1654
<212> DNA
<213> Homo sapien

```

```

<220>
<221> mutation
<222> 877
<223> A to G mutation

```

```

<221> mutation
<222> 1431
<223> G to A mutation

```

```

<221> CDS
<222> (48)...(1589)
<223> Gln277Arg/Ala462Thr Human IMPDH II mutant

```

```

<300>
<301> Farazi et al.
<302> Isolation and Characterization of Mycophenolic
<303> J. Biol. Chem. (1997)
<304> 272
<305> 2
<306> 961-965

```

```

<400> 9
gaattcgggc ggtcctcgga gacacgcggc ggtgtcctgt gttggcc atg gcc gac      56
                                     Met Ala Asp
                                     1

```

```

tac ctg att agt ggg ggc acg tcc tac gtg cca gac gac gga ctc aca      104
Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp Gly Leu Thr
      5                      10                      15

```

```

gca cag cag ctc ttc aac tgc gga gac ggc ctc acc tac aat gac ttt      152
Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr Asn Asp Phe
      20                      25                      30                      35

```

```

ctc att ctc cct ggg tac atc gac ttc act gca gac cag gtg gac ctg      200
Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln Val Asp Leu
          40                      45                      50

```

```

act tct gct ctg acc aag aaa atc act ctt aag acc cca ctg gtt tcc      248
Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro Leu Val Ser
          55                      60                      65

```

```

tct ccc atg gac aca gtc aca gag gct ggg atg gcc ata gca atg gcg      296
Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile Ala Met Ala
          70                      75                      80

```

```

ctt aca ggc ggt att ggc ttc atc cac cac aac tgt aca cct gaa ttc      344
Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr Pro Glu Phe
      85                      90                      95

```

cag gcc aat gaa gtt cgg aaa gtg aag aaa tat gaa cag gga ttc atc Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln Gly Phe Ile 100 105 110 115	392
aca gac cct gtg gtc ctc agc ccc aag gat cgc gtg cgg gat gtt ttt Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg Asp Val Phe 120 125 130	440
gag gcc aag gcc cgg cat ggt ttc tgc ggt atc cca atc aca gac aca Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile Thr Asp Thr 135 140 145	488
ggc cgg atg ggg agc cgc ttg gtg ggc atc atc tcc tcc agg gac att Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser Arg Asp Ile 150 155 160	536
gat ttt ctc aaa gag gag gaa cat gac tgt ttc ttg gaa gag ata atg Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu Glu Ile Met 165 170 175	584
aca aag agg gaa gac ttg gtg gta gcc ccc cgc agc atc aca ctg aag Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile Thr Leu Lys 180 185 190 195	632
gag gca aat gaa att ctg cag cgc agc aag aag gga aag ttg ccc att Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys Leu Pro Ile 200 205 210	680
gta aat gaa gat gat gag ctt gtg gcc atc att gcc cgg aca gac ctg Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg Thr Asp Leu 215 220 225	728
aag aag aat cgg gac tac cca cta gcc tcc aaa gat gcc aag aaa cag Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala Lys Lys Gln 230 235 240	776
ctg ctg tgt ggg gca gcc att ggc act cat gag gat gac aag tat agg Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp Lys Tyr Arg 245 250 255	824
ctg gac ttg ctc gcc cag gct ggt gtg gat gta gtg gtt ttg gac tct Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val Leu Asp Ser 260 265 270 275	872
tcc cgg gga aat tcc atc ttc cag atc aat atg atc aag tac atc aaa Ser Arg Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys Tyr Ile Lys 280 285 290	920
gac aaa tac cct aat ctc caa gtc att gga ggc aat gtg gtc act gct Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val Val Thr Ala 295 300 305	968
gcc cag gcc aag aac ctc att gat gca ggt gtg gat gcc ctg cgg gtg Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala Leu Arg Val 310 315 320	1016
ggc atg gga agt ggc tcc atc tgc att acg cag gaa gtg ctg gcc tgt Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu Ala Cys 325 330 335	1064
ggg cgg ccc caa gca aca gca gtg tac aag gtg tca gag tat gca cgg	1112

Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	Ser	Glu	Tyr	Ala	Arg		
340					345					350					355		
cgc	ttt	ggt	gtt	ccg	gtc	att	gct	gat	gga	gga	atc	caa	aat	gtg	ggg	1160	
Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Gln	Asn	Val	Gly		
				360					365					370			
cat	att	gcg	aaa	gcc	ttg	gcc	ctt	ggg	gcc	tcc	aca	gtc	atg	atg	ggc	1208	
His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val	Met	Met	Gly		
			375					380					385				
tct	ctc	ctg	gct	gcc	acc	act	gag	gcc	cct	ggt	gaa	tac	ttc	ttt	tcc	1256	
Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr	Phe	Phe	Ser		
			390				395					400					
gat	ggg	atc	cgg	cta	aag	aaa	tat	cgc	ggt	atg	ggt	tct	ctc	gat	gcc	1304	
Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met		Ser	Leu	Asp	Ala		
	405					410				415							
atg	gac	aag	cac	ctc	agc	agc	cag	aac	aga	tat	ttc	agt	gaa	gct	gac	1352	
Met	Asp	Lys	His	Leu	Ser	Ser	Gln	Asn	Arg	Tyr	Phe	Ser	Glu	Ala	Asp		
	420				425				430						435		
aaa	atc	aaa	gtg	gcc	cag	gga	gtg	tct	ggt	gct	gtg	cag	gac	aaa	ggg	1400	
Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	Val	Gln	Asp	Lys	Gly		
			440			445							450				
tca	atc	cac	aaa	ttt	gtc	cct	tac	ctg	att	act	ggc	atc	caa	cac	tca	1448	
Ser	Ile	His	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Thr	Gly	Ile	Gln	His	Ser		
			455			460						465					
tgc	cag	gac	att	ggt	gcc	aag	agc	ttg	acc	caa	gtc	cga	gcc	atg	atg	1496	
Cys	Gln	Asp	Ile	Gly	Ala	Lys	Ser	Leu	Thr	Gln	Val	Arg	Ala	Met	Met		
		470				475					480						
tac	tct	ggg	gag	ctt	aag	ttt	gag	aag	aga	acg	tcc	tca	gcc	cag	gtg	1544	
Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Ser	Ser	Ala	Gln	Val		
	485				490					495							
gaa	ggt	ggc	gtc	cat	agc	ctc	cat	tcg	tat	gag	aag	cgg	ctt	ttc		1589	
Glu	Gly	Gly	Val	His	Ser	Leu	His	Ser	Tyr	Glu	Lys	Arg	Leu	Phe			
	500				505				510								
tgaaaaggga	tccagcacac	ctcctcggtt	tttttttcaa	taaaagttta	gaaagacccg											1649	
aattc																1654	

<210> 10
 <211> 514
 <212> PRT
 <213> Homo sapien

<400> 10
 Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
 1 5 10 15
 Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
 20 25 30
 Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
 35 40 45
 Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
 50 55 60
 Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
 65 70 75 80

Ala	Met	Ala	Leu	Thr	Gly	Gly	Ile	Gly	Phe	Ile	His	His	Asn	Cys	Thr
				85					90					95	
Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Lys	Tyr	Glu	Gln
			100						105					110	
Gly	Phe	Ile	Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Lys	Asp	Arg	Val	Arg
		115					120					125			
Asp	Val	Phe	Glu	Ala	Lys	Ala	Arg	His	Gly	Phe	Cys	Gly	Ile	Pro	Ile
	130					135					140				
Thr	Asp	Thr	Gly	Arg	Met	Gly	Ser	Arg	Leu	Val	Gly	Ile	Ile	Ser	Ser
145					150					155					160
Arg	Asp	Ile	Asp	Phe	Leu	Lys	Glu	Glu	Glu	His	Asp	Cys	Phe	Leu	Glu
				165					170					175	
Glu	Ile	Met	Thr	Lys	Arg	Glu	Asp	Leu	Val	Val	Ala	Pro	Arg	Ser	Ile
			180					185					190		
Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys
	195						200					205			
Leu	Pro	Ile	Val	Asn	Glu	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg	
	210					215				220					
Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ala
225					230				235						240
Lys	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	Asp	Asp
				245					250					255	
Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Ala	Gln	Ala	Gly	Val	Asp	Val	Val	Val
			260					265					270		
Leu	Asp	Ser	Ser	Arg	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	Ile	Lys
	275					280						285			
Tyr	Ile	Lys	Asp	Lys	Tyr	Pro	Asn	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val
	290					295					300				
Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Ala
305					310					315					320
Leu	Arg	Val	Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val
				325					330					335	
Leu	Ala	Cys	Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	Ser	Glu
			340					345					350		
Tyr	Ala	Arg	Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Gln
	355						360					365			
Asn	Val	Gly	His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val
	370					375					380				
Met	Met	Gly	Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr
385					390					395					400
Phe	Phe	Ser	Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser
				405					410					415	
Leu	Asp	Ala	Met	Asp	Lys	His	Leu	Ser	Ser	Gln	Asn	Arg	Tyr	Phe	Ser
			420					425					430		
Glu	Ala	Asp	Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	Val	Gln
	435						440					445			
Asp	Lys	Gly	Ser	Ile	His	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Thr	Gly	Ile
	450					455					460				
Gln	His	Ser	Cys	Gln	Asp	Ile	Gly	Ala	Lys	Ser	Leu	Thr	Gln	Val	Arg
465					470					475					480
Ala	Met	Met	Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Ser	Ser
				485					490					495	
Ala	Gln	Val	Glu	Gly	Gly	Val	His	Ser	Leu	His	Ser	Tyr	Glu	Lys	Arg
			500					505					510		
Leu	Phe														

<210> 11
 <211> 1654
 <212> DNA
 <213> Homo sapien

```
<220>  
<221> mutation  
<222> 1414  
<223> T to C  
  
<221> mutation  
<222> 1456  
<223> A to G  
  
<221> CDS  
<222> (48)...(1589)  
<223> Phe456Ser/Asp470Gly Human IMPDH II mutant
```

```
<300>
<301> Farazi
<303> J. Biol
<304> 272
<305> 2
<306> 961-965
```

<400> 11																	
gaattcggggc ggtcctcggga gacacgcgggc ggtgtcctgt gttggcc atg gcc gac																	56
Met Ala Asp																	
1																	
tac ctg att agt ggg ggc acg tcc tac gtg cca gac gac gga ctc aca																	104
Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp Gly Leu Thr																	
5 10 15																	
gca cag cag ctc ttc aac tgc gga gac ggc ctc acc tac aat gac ttt																	152
Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr Asn Asp Phe																	
20 25 30 35																	
ctc att ctc cct ggg tac atc gac ttc act gca gac cag gtg gac ctg																	200
Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln Val Asp Leu																	
40 45 50																	
act tct gct ctg acc aag aaa atc act ctt aag acc cca ctg gtt tcc																	248
Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro Leu Val Ser																	
55 60 65																	
tct ccc atg gac aca gtc aca gag gct ggg atg gcc ata gca atg gcg																	296
Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile Ala Met Ala																	
70 75 80																	
ctt aca ggc ggt att ggc ttc atc cac cac aac tgt aca cct gaa ttc																	344
Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr Pro Glu Phe																	
85 90 95																	
cag gcc aat gaa gtt cgg aaa gtg aag aaa tat gaa cag gga ttc atc																	392
Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln Gly Phe Ile																	
100 105 110 115																	
aca gac cct gtg gtc ctc agc ccc aag gat cgc gtg cgg gat gtt ttt																	440
Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg Asp Val Phe																	
120 125 130																	
gag gcc aag gcc cgg cat ggt ttc tgc ggt atc cca atc aca gac aca																	488
Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile Thr Asp Thr																	
135 140 145																	
ggc cgg atg ggg agc cgc ttg gtg ggc atc atc tcc tcc agg gac att																	536

Gly	Arg	Met	Gly	Ser	Arg	Leu	Val	Gly	Ile	Ile	Ser	Ser	Arg	Asp	Ile	
		150					155					160				
gat	ttt	ctc	aaa	gag	gag	gaa	cat	gac	tgt	ttc	ttg	gaa	gag	ata	atg	584
Asp	Phe	Leu	Lys	Glu	Glu	Glu	His	Asp	Cys	Phe	Leu	Glu	Glu	Ile	Met	
	165					170					175					
aca	aag	agg	gaa	gac	ttg	gtg	gta	gcc	ccc	cgc	agc	atc	aca	ctg	aag	632
Thr	Lys	Arg	Glu	Asp	Leu	Val	Val	Ala	Pro	Arg	Ser	Ile	Thr	Leu	Lys	
180					185					190					195	
gag	gca	aat	gaa	att	ctg	cag	cgc	agc	aag	aag	gga	aag	ttg	ccc	att	680
Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys	Leu	Pro	Ile	
				200					205					210		
gta	aat	gaa	gat	gat	gag	ctt	gtg	gcc	atc	att	gcc	cgg	aca	gac	ctg	728
Val	Asn	Glu	Asp	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg	Thr	Asp	Leu	
			215					220					225			
aag	aag	aat	cgg	gac	tac	cca	cta	gcc	tcc	aaa	gat	gcc	aag	aaa	cag	776
Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ala	Lys	Lys	Gln	
		230				235						240				
ctg	ctg	tgt	ggg	gca	gcc	att	ggc	act	cat	gag	gat	gac	aag	tat	agg	824
Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	Asp	Asp	Lys	Tyr	Arg	
	245					250					255					
ctg	gac	ttg	ctc	gcc	cag	gct	ggc	gtg	gat	gta	gtg	gtt	ttg	gac	tct	872
Leu	Asp	Leu	Leu	Ala	Gln	Ala	Gly	Val	Asp	Val	Val	Val	Leu	Asp	Ser	
260					265					270					275	
tcc	cag	gga	aat	tcc	atc	ttc	cag	atc	aat	atg	atc	aag	tac	atc	aaa	920
Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	Ile	Lys	Tyr	Ile	Lys	
				280					285					290		
gac	aaa	tac	cct	aat	ctc	caa	gtc	att	gga	ggc	aat	gtg	gtc	act	gct	968
Asp	Lys	Tyr	Pro	Asn	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val	Val	Thr	Ala	
			295					300					305			
gcc	cag	gcc	aag	aac	ctc	att	gat	gca	ggc	gtg	gat	gcc	ctg	cgg	gtg	1016
Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Ala	Leu	Arg	Val	
		310					315					320				
ggc	atg	gga	agt	ggc	tcc	atc	tgc	att	acg	cag	gaa	gtg	ctg	gcc	tgt	1064
Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val	Leu	Ala	Cys	
	325					330					335					
ggg	cgg	ccc	caa	gca	aca	gca	gtg	tac	aag	gtg	tca	gag	tat	gca	cgg	1112
Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	Ser	Glu	Tyr	Ala	Arg	
340					345					350					355	
cgc	ttt	ggt	gtt	ccg	gtc	att	gct	gat	gga	gga	atc	caa	aat	gtg	ggt	1160
Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Gln	Asn	Val	Gly	
				360					365					370		
cat	att	gcg	aaa	gcc	ttg	gcc	ctt	ggg	gcc	tcc	aca	gtc	atg	atg	ggc	1208
His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val	Met	Met	Gly	
			375					380					385			
tct	ctc	ctg	gct	gcc	acc	act	gag	gcc	cct	ggc	gaa	tac	ttc	ttt	tcc	1256
Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr	Phe	Phe	Ser	
		390					395					400				

gat ggg atc cgg cta aag aaa tat cgc ggt atg ggt tct ctc gat gcc 1304
 Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser Leu Asp Ala
 405 410 415

atg gac aag cac ctc agc agc cag aac aga tat ttc agt gaa gct gac 1352
 Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser Glu Ala Asp
 420 425 430 435

aaa atc aaa gtg gcc cag gga gtg tct ggt gct gtg cag gac aaa ggg 1400
 Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln Asp Lys Gly
 440 445 450

tca atc cac aaa tct gtc cct tac ctg att gct ggc atc caa cac tca 1448
 Ser Ile His Lys Ser Val Pro Tyr Leu Ile Ala Gly Ile Gln His Ser
 455 460 465

tgc cag ggc att ggt gcc aag agc ttg acc caa gtc cga gcc atg atg 1496
 Cys Gln Gly Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala Met Met
 470 475 480

tac tct ggg gag ctt aag ttt gag aag aga acg tcc tca gcc cag gtg 1544
 Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala Gln Val
 485 490 495

gaa ggt ggc gtc cat agc ctc cat tcg tat gag aag cgg ctt ttc 1589
 Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu Phe
 500 505 510

tgaaaaggga tccagcacac ctccctcggtt tttttttcaa taaaagttta gaaagacccg 1649
 aattc 1654

<210> 12
 <211> 514
 <212> PRT
 <213> Homo sapien

<400> 12
 Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
 1 5 10 15
 Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
 20 25 30
 Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
 35 40 45
 Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
 50 55 60
 Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
 65 70 75 80
 Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
 85 90 95
 Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln
 100 105 110
 Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg
 115 120 125
 Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile
 130 135 140
 Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser
 145 150 155 160
 Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu
 165 170 175
 Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile
 180 185 190

```

Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
      195      200      205
Leu Pro Ile Val Asn Glu Asp Glu Leu Val Ala Ile Ile Ala Arg
      210      215      220
Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala
225      230      235      240
Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp
      245      250      255
Lys Tyr Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val
      260      265      270
Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys
      275      280      285
Tyr Ile Lys Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val
      290      295      300
Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala
305      310      315      320
Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val
      325      330      335
Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu
      340      345      350
Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln
      355      360      365
Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
      370      375      380
Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
385      390      395      400
Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
      405      410      415
Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser
      420      425      430
Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln
      435      440      445
Asp Lys Gly Ser Ile His Lys Ser Val Pro Tyr Leu Ile Ala Gly Ile
      450      455      460
Gln His Ser Cys Gln Gly Ile Gly Ala Lys Ser Leu Thr Gln Val Arg
465      470      475      480
Ala Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser
      485      490      495
Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg
      500      505      510
Leu Phe

```

```

<210> 13
<211> 1994
<212> DNA
<213> Tritrichomonas foetus

```

```

<220>
<221> CDS
<222> (115)...(1623)
<223> T. foetus IMPDH Type II

```

```

<300>
<301> Beck, J.T., Zhao, S. and Wang, C.C.
<302> Cloning, sequencing, and structural analysis of th
<303> Exp. Parasitol. (1994)
<304> 78
<305> 1
<306> 101-112

<400> 13

```

tcatatagca	aaaagccata	aacaattcaa	aacatgtatt	gaattcgtgc	atgaccatcc	60
ttcacatttc	atctcacata	gcttttttat	tttttttcatt	gtaagtccaa	acaa atg	117
					Met	
					1	
gca aaa tac tac aac gaa cca tgc cac acc ttt aac gaa tat ctc ctc	165					
Ala Lys Tyr Tyr Asn Glu Pro Cys His Thr Phe Asn Glu Tyr Leu Leu						
	5	10	15			
att cca gga ctc tca aca gtc gac tgc att cca tcc aac gtt aac tta	213					
Ile Pro Gly Leu Ser Thr Val Asp Cys Ile Pro Ser Asn Val Asn Leu						
	20	25	30			
tct acc cca ctc gtc aag ttc caa aag ggg caa caa agt gag atc aat	261					
Ser Thr Pro Leu Val Lys Phe Gln Lys Gly Gln Gln Ser Glu Ile Asn						
	35	40	45			
tta aag atc ccc ctt gtt tct gcc atc atg caa tct gtc tca gga gaa	309					
Leu Lys Ile Pro Leu Val Ser Ala Ile Met Gln Ser Val Ser Gly Glu						
	50	55	60		65	
aag atg gct atc gca ttg gca cga gaa ggt ggt att tca ttc att ttc	357					
Lys Met Ala Ile Ala Leu Ala Arg Glu Gly Gly Ile Ser Phe Ile Phe						
	70	75	80			
gga tct caa tca att gaa agc caa gca gcc atg gtc cat gct gtc aaa	405					
Gly Ser Gln Ser Ile Glu Ser Gln Ala Ala Met Val His Ala Val Lys						
	85	90	95			
aat ttc aaa gcc ggc ttt gtc gtc tca gat tca aac gtt aaa cca gat	453					
Asn Phe Lys Ala Gly Phe Val Val Ser Asp Ser Asn Val Lys Pro Asp						
	100	105	110			
caa aca ttt gct gat gtt tta gca att tct caa cga aca acc cac aac	501					
Gln Thr Phe Ala Asp Val Leu Ala Ile Ser Gln Arg Thr Thr His Asn						
	115	120	125			
act gtc gct gtc aca gac gat gga act cca cat gga gtt tta ctt ggt	549					
Thr Val Ala Val Thr Asp Asp Gly Thr Pro His Gly Val Leu Leu Gly						
	130	135	140		145	
ttg gtc act caa cgc gat tat cca atc gat ctt acc cag acc gaa aca	597					
Leu Val Thr Gln Arg Asp Tyr Pro Ile Asp Leu Thr Gln Thr Glu Thr						
	150	155	160			
aag gtt tcc gac atg atg aca cca ttc agc aag ctc gtt aca gcc cat	645					
Lys Val Ser Asp Met Met Thr Pro Phe Ser Lys Leu Val Thr Ala His						
	165	170	175			
cag gac aca aaa ctt tca gaa gcc aac aaa att att tgg gag aag aaa	693					
Gln Asp Thr Lys Leu Ser Glu Ala Asn Lys Ile Ile Trp Glu Lys Lys						
	180	185	190			
tta aat gct ctt cct atc att gat gac gat caa cat ctt cgt tat atc	741					
Leu Asn Ala Leu Pro Ile Ile Asp Asp Asp Gln His Leu Arg Tyr Ile						
	195	200	205			
gtt ttc cgc aaa gat tat gac aga tcg caa gtc tgt cac aac gaa ctc	789					
Val Phe Arg Lys Asp Tyr Asp Arg Ser Gln Val Cys His Asn Glu Leu						
	210	215	220		225	
gtc gat tcg caa aaa cgc tat ttg gtc gga gca gga att aac aca cgc	837					

Val	Asp	Ser	Gln	Lys	Arg	Tyr	Leu	Val	Gly	Ala	Gly	Ile	Asn	Thr	Arg	
				230					235					240		
gac	ttc	aga	gaa	cgc	gtt	cca	gca	ctt	gtc	gaa	gcc	ggc	gct	gat	gtc	885
Asp	Phe	Arg	Glu	Arg	Val	Pro	Ala	Leu	Val	Glu	Ala	Gly	Ala	Asp	Val	
			245					250					255			
ctt	tgc	att	gat	tcc	agc	gac	ggc	ttc	tca	gaa	tgg	cag	aaa	att	aca	933
Leu	Cys	Ile	Asp	Ser	Ser	Asp	Gly	Phe	Ser	Glu	Trp	Gln	Lys	Ile	Thr	
		260					265					270				
atc	ggc	tgg	att	cgc	gag	aaa	tac	ggc	gat	aaa	gtt	aaa	gtt	ggg	gcg	981
Ile	Gly	Trp	Ile	Arg	Glu	Lys	Tyr	Gly	Asp	Lys	Val	Lys	Val	Gly	Ala	
	275					280					285					
gga	aac	att	gtt	gac	ggt	gaa	gga	ttc	cgc	tat	ttg	gcc	gac	gct	gga	1029
Gly	Asn	Ile	Val	Asp	Gly	Glu	Gly	Phe	Arg	Tyr	Leu	Ala	Asp	Ala	Gly	
	290				295				300						305	
gct	gat	ttc	atc	aag	att	gga	att	ggc	ggg	gga	tca	att	tgc	atc	aca	1077
Ala	Asp	Phe	Ile	Lys	Ile	Gly	Ile	Gly	Gly	Gly	Ser	Ile	Cys	Ile	Thr	
				310				315						320		
cgc	gag	cag	aaa	ggt	atc	ggc	cga	ggc	caa	gct	act	gcc	gtc	att	gat	1125
Arg	Glu	Gln	Lys	Gly	Ile	Gly	Arg	Gly	Gln	Ala	Thr	Ala	Val	Ile	Asp	
			325				330						335			
gtt	gtt	gca	gag	cgt	aac	aaa	tac	ttc	gaa	gag	acc	gga	att	tat	atc	1173
Val	Val	Ala	Glu	Arg	Asn	Lys	Tyr	Phe	Glu	Glu	Thr	Gly	Ile	Tyr	Ile	
		340				345						350				
cct	gtt	tgc	tct	gat	ggt	gga	att	gtt	tat	gat	tat	cac	atg	aca	ctt	1221
Pro	Val	Cys	Ser	Asp	Gly	Gly	Ile	Val	Tyr	Asp	Tyr	His	Met	Thr	Leu	
	355				360						365					
gct	ctt	gca	atg	ggc	gca	gat	ttc	atc	atg	ctt	ggc	agg	tac	ttc	gcc	1269
Ala	Leu	Ala	Met	Gly	Ala	Asp	Phe	Ile	Met	Leu	Gly	Arg	Tyr	Phe	Ala	
	370				375					380					385	
cgt	ttt	gag	gag	tca	cca	aca	aga	aaa	gtg	aca	att	aat	gga	agc	gtt	1317
Arg	Phe	Glu	Glu	Ser	Pro	Thr	Arg	Lys	Val	Thr	Ile	Asn	Gly	Ser	Val	
				390					395					400		
atg	aag	gag	tac	tgg	gga	gaa	ggc	tct	tcg	cgc	gct	agg	aac	tgg	cag	1365
Met	Lys	Glu	Tyr	Trp	Gly	Glu	Gly	Ser	Ser	Arg	Ala	Arg	Asn	Trp	Gln	
			405				410						415			
cgc	tat	gac	ctt	gga	ggt	aag	cag	aag	ctt	tcc	ttt	gaa	gag	gga	gtc	1413
Arg	Tyr	Asp	Leu	Gly	Gly	Lys	Gln	Lys	Leu	Ser	Phe	Glu	Glu	Gly	Val	
		420					425					430				
gat	tct	tac	gtc	cca	tac	gct	gga	aag	ttg	aag	gac	aac	gtg	gag	gca	1461
Asp	Ser	Tyr	Val	Pro	Tyr	Ala	Gly	Lys	Leu	Lys	Asp	Asn	Val	Glu	Ala	
		435				440					445					
tcc	ttg	aac	aag	gta	aaa	tca	acg	atg	tgc	aac	tgt	gga	gcg	ctc	aca	1509
Ser	Leu	Asn	Lys	Val	Lys	Ser	Thr	Met	Cys	Asn	Cys	Gly	Ala	Leu	Thr	
	450				455					460					465	
atc	ccg	cag	ctc	cag	agc	aag	gca	aag	atc	aca	ctt	gta	tca	tca	gtt	1557
Ile	Pro	Gln	Leu	Gln	Ser	Lys	Ala	Lys	Ile	Thr	Leu	Val	Ser	Ser	Val	
				470					475						480	

tca	att	gtc	gaa	gga	ggc	gca	cac	gat	gtt	att	gtt	aag	gac	agg	att	1605
Ser	Ile	Val	Glu	Gly	Gly	Ala	His	Asp	Val	Ile	Val	Lys	Asp	Arg	Ile	
			485					490					495			

aac gac tat cac cca aaa taaatatatt gttttatact ttatgtttgt 1653
Asn Asp Tyr His Pro Lys
500

taaattatac	ctattttactt	ctcttgtttt	tatgtctttt	gattcttcca	tgtctttgaa	1713
ttcttccatg	tcttttgatt	ctttttccca	catgggtgat	gtgttggaatt	attcaaaacc	1773
cttttccttt	gtaacttgtc	attaattggc	attttcggag	tgaactagtt	aattattttt	1833
ccaatgatat	ttatttatagt	cttttttgtgt	attgatgtct	tactttactg	atagtgatta	1893
ggtcaataact	ctattatgga	gtctgactcg	cgttactcta	tctatatataa	ctataacaca	1953
tagctttaqtc	tacactgcqt	agctctttqt	acctgacatg	a		1994

```
<210> 14
<211> 503
<212> PRT
<213> Tritrichomonas foetus
```

<400>	14															
Met	Ala	Lys	Tyr	Tyr	Asn	Glu	Pro	Cys	His	Thr	Phe	Asn	Glu	Tyr	Leu	
1				5					10					15		
Leu	Ile	Pro	Gly	Leu	Ser	Thr	Val	Asp	Cys	Ile	Pro	Ser	Asn	Val	Asn	
			20					25					30			
Leu	Ser	Thr	Pro	Leu	Val	Lys	Phe	Gln	Lys	Gly	Gln	Gln	Ser	Glu	Ile	
		35					40					45				
Asn	Leu	Lys	Ile	Pro	Leu	Val	Ser	Ala	Ile	Met	Gln	Ser	Val	Ser	Gly	
	50					55					60					
Glu	Lys	Met	Ala	Ile	Ala	Leu	Ala	Arg	Glu	Gly	Gly	Ile	Ser	Phe	Ile	
65					70					75					80	
Phe	Gly	Ser	Gln	Ser	Ile	Glu	Ser	Gln	Ala	Ala	Met	Val	His	Ala	Val	
				85					90					95		
Lys	Asn	Phe	Lys	Ala	Gly	Phe	Val	Val	Ser	Asp	Ser	Asn	Val	Lys	Pro	
			100					105					110			
Asp	Gln	Thr	Phe	Ala	Asp	Val	Leu	Ala	Ile	Ser	Gln	Arg	Thr	Thr	His	
		115					120					125				
Asn	Thr	Val	Ala	Val	Thr	Asp	Asp	Gly	Thr	Pro	His	Gly	Val	Leu	Leu	
		130				135					140					
Gly	Leu	Val	Thr	Gln	Arg	Asp	Tyr	Pro	Ile	Asp	Leu	Thr	Gln	Thr	Glu	
145					150					155					160	
Thr	Lys	Val	Ser	Asp	Met	Met	Thr	Pro	Phe	Ser	Lys	Leu	Val	Thr	Ala	
				165					170						175	
His	Gln	Asp	Thr	Lys	Leu	Ser	Glu	Ala	Asn	Lys	Ile	Ile	Trp	Glu	Lys	
			180					185					190			
Lys	Leu	Asn	Ala	Leu	Pro	Ile	Ile	Asp	Asp	Asp	Gln	His	Leu	Arg	Tyr	
		195					200					205				
Ile	Val	Phe	Arg	Lys	Asp	Tyr	Asp	Arg	Ser	Gln	Val	Cys	His	Asn	Glu	
	210					215					220					
Leu	Val	Asp	Ser	Gln	Lys	Arg	Tyr	Leu	Val	Gly	Ala	Gly	Ile	Asn	Thr	
225					230					235					240	
Arg	Asp	Phe	Arg	Glu	Arg	Val	Pro	Ala	Leu	Val	Glu	Ala	Gly	Ala	Asp	
				245					250					255		
Val	Leu	Cys	Ile	Asp	Ser	Ser	Asp	Gly	Phe	Ser	Glu	Trp	Gln	Lys	Ile	
			260					265					270			
Thr	Ile	Gly	Trp	Ile	Arg	Glu	Lys	Tyr	Gly	Asp	Lys	Val	Lys	Val	Gly	
		275					280					285				
Ala	Gly	Asn	Ile	Val	Asp	Gly	Glu	Gly	Phe	Arg	Tyr	Leu	Ala	Asp	Ala	
	290					295					300					
Gly	Ala	Asp	Phe	Ile	Lys	Ile	Gly	Ile	Gly	Gly	Gly	Ser	Ile	Cys	Ile	
305					310					315					320	

Thr Arg Glu Gln Lys Gly Ile Gly Arg Gly Gln Ala Thr Ala Val Ile
 325 330 335
 Asp Val Val Ala Glu Arg Asn Lys Tyr Phe Glu Glu Thr Gly Ile Tyr
 340 345 350
 Ile Pro Val Cys Ser Asp Gly Gly Ile Val Tyr Asp Tyr His Met Thr
 355 360 365
 Leu Ala Leu Ala Met Gly Ala Asp Phe Ile Met Leu Gly Arg Tyr Phe
 370 375 380
 Ala Arg Phe Glu Glu Ser Pro Thr Arg Lys Val Thr Ile Asn Gly Ser
 385 390 395 400
 Val Met Lys Glu Tyr Trp Gly Glu Gly Ser Ser Arg Ala Arg Asn Trp
 405 410 415
 Gln Arg Tyr Asp Leu Gly Gly Lys Gln Lys Leu Ser Phe Glu Glu Gly
 420 425 430
 Val Asp Ser Tyr Val Pro Tyr Ala Gly Lys Leu Lys Asp Asn Val Glu
 435 440 445
 Ala Ser Leu Asn Lys Val Lys Ser Thr Met Cys Asn Cys Gly Ala Leu
 450 455 460
 Thr Ile Pro Gln Leu Gln Ser Lys Ala Lys Ile Thr Leu Val Ser Ser
 465 470 475 480
 Val Ser Ile Val Glu Gly Gly Ala His Asp Val Ile Val Lys Asp Arg
 485 490 495
 Ile Asn Asp Tyr His Pro Lys
 500

<210> 15
 <211> 1560
 <212> DNA
 <213> *Aspergillus nidulans*
 <220>
 <221> CDS
 <222> (1)...(1560)
 <223> *Aspergillus nidulans* wild type DHODH cDNA

<400> 15
 atg gct acg aat tct ttc cga aaa ctc act ttt tca gga gcc tcc cgt 48
 Met Ala Thr Asn Ser Phe Arg Lys Leu Thr Phe Ser Gly Ala Ser Arg
 1 5 10 15
 ctg ggt ggt tgt cgc cgt ctc cca cta acc tgc aga caa ctt cga ttc 96
 Leu Gly Gly Cys Arg Arg Leu Pro Leu Thr Cys Arg Gln Leu Arg Phe
 20 25 30
 gcc tcc gac agc gga gcc gca gcg gca act aca aaa gca acg gcc gaa 144
 Ala Ser Asp Ser Gly Ala Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu
 35 40 45
 tca gca gcc gag tca gct agt ata aac gtc aaa gag gca ccc aaa aag 192
 Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys
 50 55 60
 gcc gga cgg ggc ctg cgg cgc acg gtc ctg gga acg tcg ttg gcg ctg 240
 Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu
 65 70 75 80
 acg ctg ctg gtt gga tat gtc tac ggg acg gac acc cgg gcg agt gtg 288
 Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val
 85 90 95
 cat cgg tac ggt gtt gtg ccg ctg att aga gca ttg tat cct gat gcg 336
 His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala

100					105					110						
gaa	gat	gcg	cat	cat	att	ggg	gtc	gat	act	tta	aag	atg	ctg	tat	aag	384
Glu	Asp	Ala	His	His	Ile	Gly	Val	Asp	Thr	Leu	Lys	Met	Leu	Tyr	Lys	
		115					120					125				
tat	ggg	ctg	cat	cca	agg	gaa	cgg	ggg	gat	ccg	gat	gga	gat	ggg	gcg	432
Tyr	Gly	Leu	His	Pro	Arg	Glu	Arg	Gly	Asp	Pro	Asp	Gly	Asp	Gly	Ala	
	130					135					140					
ctg	gcg	aca	gag	gtc	ttt	ggg	tat	aca	ctg	tca	aac	cca	att	ggc	ata	480
Leu	Ala	Thr	Glu	Val	Phe	Gly	Tyr	Thr	Leu	Ser	Asn	Pro	Ile	Gly	Ile	
145					150					155					160	
tcg	ggc	ggc	ctg	gac	aag	cat	gct	gag	atc	cct	gat	ccg	ctg	ttc	gcg	528
Ser	Gly	Gly	Leu	Asp	Lys	His	Ala	Glu	Ile	Pro	Asp	Pro	Leu	Phe	Ala	
				165					170					175		
atc	ggg	cct	gcc	att	gtc	gaa	gtc	ggg	ggg	acg	aca	ccc	tta	cca	cag	576
Ile	Gly	Pro	Ala	Ile	Val	Glu	Val	Gly	Gly	Thr	Thr	Pro	Leu	Pro	Gln	
			180					185					190			
gat	ggg	aac	ccg	cgt	cct	cgc	gta	ttc	cga	ctt	cca	tca	cag	aga	gcg	624
Asp	Gly	Asn	Pro	Arg	Pro	Arg	Val	Phe	Arg	Leu	Pro	Ser	Gln	Arg	Ala	
		195					200					205				
atg	ata	aac	cgg	tac	ggc	ctc	aac	tcc	aaa	ggc	gca	gat	cac	atg	gca	672
Met	Ile	Asn	Arg	Tyr	Gly	Leu	Asn	Ser	Lys	Gly	Ala	Asp	His	Met	Ala	
	210					215					220					
gct	atc	ttg	gag	caa	cga	gta	cgc	gat	ttt	gcc	tac	gca	aac	gga	ttt	720
Ala	Ile	Leu	Glu	Gln	Arg	Val	Arg	Asp	Phe	Ala	Tyr	Ala	Asn	Gly	Phe	
225					230					235					240	
ggg	gca	tac	gat	gcg	gct	aag	cag	cgt	gta	ttg	gac	ggc	gaa	gct	ggg	768
Gly	Ala	Tyr	Asp	Ala	Ala	Lys	Gln	Arg	Val	Leu	Asp	Gly	Glu	Ala	Gly	
				245					250					255		
gtg	cca	cca	ggg	agt	ctt	cag	cct	ggg	aag	ctt	tta	gct	gtc	caa	gtg	816
Val	Pro	Pro	Gly	Ser	Leu	Gln	Pro	Gly	Lys	Leu	Leu	Ala	Val	Gln	Val	
			260					265					270			
gca	aag	aac	aag	gcc	act	cct	gac	ggc	gac	att	gaa	gcc	atc	aag	cgc	864
Ala	Lys	Asn	Lys	Ala	Thr	Pro	Asp	Gly	Asp	Ile	Glu	Ala	Ile	Lys	Arg	
		275					280					285				
gac	tat	gtg	tat	tgc	gtg	gac	cgt	gtg	gcc	aaa	tac	gct	gat	att	ctt	912
Asp	Tyr	Val	Tyr	Cys	Val	Asp	Arg	Val	Ala	Lys	Tyr	Ala	Asp	Ile	Leu	
	290					295					300					
gtt	gtg	aat	gta	tgc	agc	ccc	aac	aca	ccc	ggg	ctc	cgt	gac	ctt	caa	960
Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Pro	Gly	Leu	Arg	Asp	Leu	Gln	
305					310					315					320	
gcc	act	gcc	ccg	ctc	aca	gct	atc	ttg	agt	gct	gtc	gtt	ggc	gcg	gca	1008
Ala	Thr	Ala	Pro	Leu	Thr	Ala	Ile	Leu	Ser	Ala	Val	Val	Gly	Ala	Ala	
				325					330					335		
aag	agc	gtg	aac	cgc	aag	acc	aaa	cca	tat	gtt	atg	gtc	aag	gtc	agt	1056
Lys	Ser	Val	Asn	Arg	Lys	Thr	Lys	Pro	Tyr	Val	Met	Val	Lys	Val	Ser	
			340					345					350			

ccg gat gaa gac tca gat gaa caa gtc tct ggt atc tgc gac gcc gtc	1104
Pro Asp Glu Asp Ser Asp Glu Gln Val Ser Gly Ile Cys Asp Ala Val	
355 360 365	
cga gca tcc ggt gtc gac gga gtg att gtc gga aac aca aca aac cgt	1152
Arg Ala Ser Gly Val Asp Gly Val Ile Val Gly Asn Thr Thr Asn Arg	
370 375 380	
cgc ccc gac cct ata ccc caa ggt tac act ctt ccg gcc aag gag cag	1200
Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln	
385 390 395 400	
gca acg ttg aaa gaa acc ggc ggg tat tca ggt cca cag ctg ttc gat	1248
Ala Thr Leu Lys Glu Thr Gly Gly Tyr Ser Gly Pro Gln Leu Phe Asp	
405 410 415	
cgc aca gtg gcc ctt gtg gct cgg tac cgc tcc atg ctg gat gcg gag	1296
Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Asp Ala Glu	
420 425 430	
tcg gaa acg gcc gga tcc gcc aag gat tca gca gcg acc ata gcg caa	1344
Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln	
435 440 445	
aca gag cca ggc tcg gaa aac gtt cct cct gtg gaa gcg cca agc gga	1392
Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly	
450 455 460	
ctg ccg cgc aaa gtt atc ttc gct tcg ggt ggt atc acc aac ggg aag	1440
Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys	
465 470 475 480	
cag gct cac gct gtt tta gac aca ggg gca tct gtt gcc atg atg tac	1488
Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr	
485 490 495	
acc ggt gtg gtc tat ggt ggc gtc ggc act gtc act cga gtg aag caa	1536
Thr Gly Val Val Tyr Gly Gly Val Gly Thr Val Thr Arg Val Lys Gln	
500 505 510	
gaa ctt cga acg gcg aaa aag gag	1560
Glu Leu Arg Thr Ala Lys Lys Glu	
515 520	

<210> 16

<211> 520

<212> PRT

<213> Aspergillus nidulans

<400> 16

Met Ala Thr Asn Ser Phe Arg Lys Leu Thr Phe Ser Gly Ala Ser Arg	
1 5 10 15	
Leu Gly Gly Cys Arg Arg Leu Pro Leu Thr Cys Arg Gln Leu Arg Phe	
20 25 30	
Ala Ser Asp Ser Gly Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu	
35 40 45	
Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys	
50 55 60	
Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu	
65 70 75 80	
Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val	

<221> CDS
 <222> (601)...(2142)
 <223> Human wild-type IMPDH type I

<300>
 <301> Natsumeda et al.
 <302> Two Distinct cDNAs for Human IMP Dehydrogenase
 <303> J. Biol. Chem. (1990)
 <304> 265
 <305> 9
 <306> 5292-5295

<400> 17
 tcggaagggg ccaggagaca ctggaagggtc cggacggcag ggaaggggac ggggttcttt 60
 ccagtcccac ccgtgtaggg acacctctcc ccctcatccc ccgatgtacc ctgctgaat 120
 ctgggatggg agagacgaac cgagtctagg catctgcgta gcagcgccgg ggagagcggg 180
 gagcccaggc ggagcccagt cgactcccgg attcccctgc cccgcccccg gcacgaggcc 240
 ccgccccggc gccccgcccc tctctgggac tcgaccgggc tgcgctcact gcccagccgg 300
 ggccccggga gcctccaggc tcgcccggcc tgagctgcgg cctccgcatt gagggccact 360
 cactccacca ccgctgcagg gaggcggacg gcgctgttcc ggagcccggg gcccggcaac 420
 acccgggaca cgagacggcg gcgcagggct acagcgcccg actgctgcag gccggctacg 480
 agcccgagag ccctagattg gacctcgcta cacaccgac gacaccccg tcagaactat 540
 cttcagtggg cttactggca ggtgttggtg tccagatgga tcgccttcgc agggctagcc 600
 atg gcg gac tac ctg atc agc ggc ggc acc ggc tac gtg ccc gag gat 648
 Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Gly Tyr Val Pro Glu Asp
 1 5 10 15
 ggg ctc acc gcg cag cag ctc ttc gcc agc gcc gac gac ctc acc tac 696
 Gly Leu Thr Ala Gln Gln Leu Phe Ala Ser Ala Asp Asp Leu Thr Tyr
 20 25 30
 aac gac ttc ctg att ctc cca gga ttc ata gac ttc ata gct gat gag 744
 Asn Asp Phe Leu Ile Leu Pro Gly Phe Ile Asp Phe Ile Ala Asp Glu
 35 40 45
 gtg gac ctg acc tca gcc ctg acc cgg aag atc acg ctg aag acg cca 792
 Val Asp Leu Thr Ser Ala Leu Thr Arg Lys Ile Thr Leu Lys Thr Pro
 50 55 60
 ctc atc tcc tcc ccc atg gac act gtg aca gag gct gac atg gcc att 840
 Leu Ile Ser Ser Pro Met Asp Thr Val Thr Glu Ala Asp Met Ala Ile
 65 70 75 80
 gcc atg gct ctg atg gga ggt att ggg ttc att cac cac aac tgc acc 888
 Ala Met Ala Leu Met Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
 85 90 95
 cca gag ttc cag gcc aat gaa gta cgc aag gtc aag aac ttt gaa cag 936
 Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Asn Phe Glu Gln
 100 105 110
 ggc ttc atc acg gac cct gtg gtg ctg agc ccc tcg cac act gtg ggc 984
 Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Ser His Thr Val Gly
 115 120 125
 gat gtg ctg gag gcc aag atg cgg cat ggc ttc tct ggc atc ccc atc 1032
 Asp Val Leu Glu Ala Lys Met Arg His Gly Phe Ser Gly Ile Pro Ile
 130 135 140
 act gag acg ggc acc atg ggc agc aag ctg gtg ggc atc gtc acc tcc 1080
 Thr Glu Thr Gly Thr Met Gly Ser Lys Leu Val Gly Ile Val Thr Ser
 145 150 155 160

cga gac atc gac ttt ctt gct gag aag gac cac acc acc ctc ctc agt Arg Asp Ile Asp Phe Leu Ala Glu Lys Asp His Thr Thr Leu Leu Ser 165 170 175	1128
gag gtg atg acg cca agg att gaa ctg gtg gtg gct cca gca ggt gtg Glu Val Met Thr Pro Arg Ile Glu Leu Val Val Ala Pro Ala Gly Val 180 185 190	1176
acg ttg aaa gag gca aat gag atc ctg cag cgt agc aag aaa ggg aag Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys 195 200 205	1224
ctg cct atc gtc aat gat tgc gat gag ctg gtg gcc atc atc gcc cgc Leu Pro Ile Val Asn Asp Cys Asp Glu Leu Val Ala Ile Ile Ala Arg 210 215 220	1272
acc gac ctg aag aag aat cga gac tac cct ctg gcc tcc aag gat tcc Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ser 225 230 235 240	1320
cag aag cag ctg ctc tgt ggg gca gct gtg ggc acc cgt gag gat gac Gln Lys Gln Leu Leu Cys Gly Ala Ala Val Gly Thr Arg Glu Asp Asp 245 250 255	1368
aaa tac cgt ctg gac ctg ctg acc cag gcg ggg gtc gac gtc ata gtc Lys Tyr Arg Leu Asp Leu Leu Thr Gln Ala Gly Val Asp Val Ile Val 260 265 270	1416
ttc cac tcg tcc caa ggg aat tcg gtg tat cag atc gcc atg gtg cat Phe His Ser Ser Gln Gly Asn Ser Val Tyr Gln Ile Ala Met Val His 275 280 285	1464
tac atc aaa cag aag tac ccc cac ctc cag gtg att ggg ggg aac gtg Tyr Ile Lys Gln Lys Tyr Pro His Leu Gln Val Ile Gly Gly Asn Val 290 295 300	1512
gtg aca gca gcc cag gcc aag aac ctg att gat gct ggt gtg gac ggg Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Gly 305 310 315 320	1560
ctg cgc gtg ggc atg ggc tgc ggc tcc atc tgc atc acc cag gaa gtg Leu Arg Val Gly Met Gly Cys Gly Ser Ile Cys Ile Thr Gln Glu Val 325 330 335	1608
atg gcc tgt ggt cgg ccc cag ggc act gct gtg tac aag gtg gct gag Met Ala Cys Gly Arg Pro Gln Gly Thr Ala Val Tyr Lys Val Ala Glu 340 345 350	1656
tat gcc cgg cgc ttt ggt gtg ccc atc ata gcc gat ggc ggc atc cag Tyr Ala Arg Arg Phe Gly Val Pro Ile Ile Ala Asp Gly Gly Ile Gln 355 360 365	1704
acc gtg gga cac gtg gtc aag gcc ctg gcc ctt gga gcc tcc aca gtg Thr Val Gly His Val Val Lys Ala Leu Ala Leu Gly Ala Ser Thr Val 370 375 380	1752
atg atg ggc tcc ctg ctg gcc gcc act acg gag gcc cct ggc gag tac Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr 385 390 395 400	1800
ttc ttc tca gac ggg gtg cgg ctc aag aag tac cgg ggc atg ggc tca	1848

Phe Phe Ser Asp Gly Val Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
 405 410 415
 ctg gat ccc atg gag aag agc agc agc agc cag aaa cga tac ttc agc 1896
 Leu Asp Pro Met Glu Lys Ser Ser Ser Ser Gln Lys Arg Tyr Phe Ser
 420 425 430
 gag ggg gat aaa gtg aag atc gca cag ggt gtc tcg ggc tcc atc cag 1944
 Glu Gly Asp Lys Val Lys Ile Ala Gln Gly Val Ser Gly Ser Ile Gln
 435 440 445
 gac aaa gga tcc att cag aag ttc gtg ccc tac ctc ata gca ggc atc 1992
 Asp Lys Gly Ser Ile Gln Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile
 450 455 460
 caa cac ggc tgc cag gat atc ggg gcc cgc agc ctg tct gtc ctt cgg 2040
 Gln His Gly Cys Gln Asp Ile Gly Ala Arg Ser Leu Ser Val Leu Arg
 465 470 475 480
 tcc atg atg tac tca gga gag ctc aag ttt gag aag cgg acc atg tcg 2088
 Ser Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Met Ser
 485 490 495
 ccc cag att gag ggt ggt gtc cat ggc ctg cac tct tac gaa aag cgg 2136
 Pro Gln Ile Glu Gly Gly Val His Gly Leu His Ser Tyr Glu Lys Arg
 500 505 510
 ctg tac tgaggacagc ggtggaggcc gaggtggtgg aggggatgca cccagtgctc 2192
 Leu Tyr
 cacttttggg cacaggctcc ctccataact gagtgggtcca cagatttgca ctacgggttc 2252
 tccagctcct ttccaggcag agaggagggg aggtcctgag gggactgctg cccctcactc 2312
 ggcattcccct gcagagtcag gactgctccc gggggccagg ctgccctggg aggcccccctc 2372
 cgagaccagc cagccaggct ctcaggacct gcgctgcctt aggatctttc ttgctgcagc 2432
 ctgctccagc ctggccccc cccagggggc aggcggccccc tccctggcttc tcctgtaggg 2492
 cacctccctg cccctagcct cccagcaaat ggtgctctcc tggccctgct ctggcccttc 2552
 ccgggcccgtg cccctcagcc atgtggcact tctgagctcc tgacctaggc caagggggagg 2612
 tctctgcccc ctccccggc cctggggtac ccttgggtcc tgcctcctcag gccgctcccc 2672
 tgtccctggc catgggtagg agactgcctt ggtcatggcc gcctgcctgt cattcctgac 2732
 tcaccaccgt cccagggtga accattcctc ccttctcctc agctgcagtc gaaggcttta 2792
 actttgcaca cttgggatca cagttgcgtc attgtgtatt aaatacttgg aataaatcaa 2852
 gcaggt 2858

<210> 18
 <211> 514
 <212> PRT
 <213> Homo sapien

<400> 18
 Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Gly Tyr Val Pro Glu Asp
 1 5 10 15
 Gly Leu Thr Ala Gln Gln Leu Phe Ala Ser Ala Asp Asp Leu Thr Tyr
 20 25 30
 Asn Asp Phe Leu Ile Leu Pro Gly Phe Ile Asp Phe Ile Ala Asp Glu
 35 40 45
 Val Asp Leu Thr Ser Ala Leu Thr Arg Lys Ile Thr Leu Lys Thr Pro
 50 55 60
 Leu Ile Ser Ser Pro Met Asp Thr Val Thr Glu Ala Asp Met Ala Ile
 65 70 75 80
 Ala Met Ala Leu Met Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
 85 90 95

```

Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Asn Phe Glu Gln
      100      105      110
Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Ser His Thr Val Gly
      115      120      125
Asp Val Leu Glu Ala Lys Met Arg His Gly Phe Ser Gly Ile Pro Ile
      130      135      140
Thr Glu Thr Gly Thr Met Gly Ser Lys Leu Val Gly Ile Val Thr Ser
145      150      155      160
Arg Asp Ile Asp Phe Leu Ala Glu Lys Asp His Thr Thr Leu Leu Ser
      165      170      175
Glu Val Met Thr Pro Arg Ile Glu Leu Val Val Ala Pro Ala Gly Val
      180      185      190
Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
      195      200      205
Leu Pro Ile Val Asn Asp Cys Asp Glu Leu Val Ala Ile Ile Ala Arg
210      215      220
Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ser
225      230      235      240
Gln Lys Gln Leu Leu Cys Gly Ala Ala Val Gly Thr Arg Glu Asp Asp
      245      250      255
Lys Tyr Arg Leu Asp Leu Leu Thr Gln Ala Gly Val Asp Val Ile Val
      260      265      270
Phe His Ser Ser Gln Gly Asn Ser Val Tyr Gln Ile Ala Met Val His
      275      280      285
Tyr Ile Lys Gln Lys Tyr Pro His Leu Gln Val Ile Gly Gly Asn Val
290      295      300
Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Gly
305      310      315      320
Leu Arg Val Gly Met Gly Cys Gly Ser Ile Cys Ile Thr Gln Glu Val
      325      330      335
Met Ala Cys Gly Arg Pro Gln Gly Thr Ala Val Tyr Lys Val Ala Glu
      340      345      350
Tyr Ala Arg Arg Phe Gly Val Pro Ile Ile Ala Asp Gly Gly Ile Gln
      355      360      365
Thr Val Gly His Val Val Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
      370      375      380
Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
385      390      395      400
Phe Phe Ser Asp Gly Val Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
      405      410      415
Leu Asp Pro Met Glu Lys Ser Ser Ser Gln Lys Arg Tyr Phe Ser
      420      425      430
Glu Gly Asp Lys Val Lys Ile Ala Gln Gly Val Ser Gly Ser Ile Gln
      435      440      445
Asp Lys Gly Ser Ile Gln Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile
      450      455      460
Gln His Gly Cys Gln Asp Ile Gly Ala Arg Ser Leu Ser Val Leu Arg
465      470      475      480
Ser Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Met Ser
      485      490      495
Pro Gln Ile Glu Gly Gly Val His Gly Leu His Ser Tyr Glu Lys Arg
      500      505      510
Leu Tyr

```

```

<210> 19
<211> 1496
<212> DNA
<213> Homo sapien

```

```

<220>
<221> CDS

```

<222> (0)...(1188)

<223> Human wild-type Dihydroorotate Dehydrogenase
(DHODH) "PYRDH" cDNA clone

<300>

<301> Minet, M., Dufour, M-E., and Lacroute, F.

<302> Cloning and Sequencing of a Human cDNA coding for

<303> Gene (1992)

<304> 121

<306> 393-396

<400> 19

aaa tta ccg tgg aga cac ctg caa aag cgg gcc cag gat gct gtg atc	48
Lys Leu Pro Trp Arg His Leu Gln Lys Arg Ala Gln Asp Ala Val Ile	
1 5 10 15	
atc ctg ggg gga gga gga ctt ctc ttc gcc tcc tac ctg atg gcc acg	96
Ile Leu Gly Gly Gly Leu Leu Phe Ala Ser Tyr Leu Met Ala Thr	
20 25 30	
gga gat gag cgt ttc tat gct gaa cac ctg atg ccg act ctg cag ggg	144
Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr Leu Gln Gly	
35 40 45	
ctg ctg gac ccg gag tca gcc cac aga ctg gct gtt cgc ttc acc tcc	192
Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg Phe Thr Ser	
50 55 60	
ctg ggg ctc ctt cca cgg gcc aga ttt caa gac tct gac atg ctg gaa	240
Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp Met Leu Glu	
65 70 75 80	
gtg aga gtt ctg ggc cat aaa ttc cga aat cca gta gga att gct gca	288
Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly Ile Ala Ala	
85 90 95	
gga ttt gac aag cat ggg gaa gcc gtg gac gga ctt tat aag atg ggc	336
Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr Lys Met Gly	
100 105 110	
ttt ggt ttt gtt gag ata gga agt gtg act cca aaa cct cag gaa gga	384
Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro Gln Glu Gly	
115 120 125	
aac cct aga ccc aga gtc ttc cgc ctc cct gag gac caa gct gtc att	432
Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln Ala Val Ile	
130 135 140	
aac agg tat gga ttt aac agt cac ggg ctt tca gtg gtg gaa cac agg	480
Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val Glu His Arg	
145 150 155 160	
tta cgg gcc aga cag cag aag cag gcc aag ctc aca gaa gat gga ctg	528
Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu Asp Gly Leu	
165 170 175	
cct ctg ggg gtc aac ttg ggg aag aac aag acc tca gtg gac gcc gcg	576
Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val Asp Ala Ala	
180 185 190	
gag gac tac gca gaa ggg gtg cgc gta ctg ggc ccc ctg gcc gac tac	624
Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu Ala Asp Tyr	

195					200					205						
ctg	gtg	gtg	aat	gtg	tcc	agc	ccc	aac	act	gcc	ggg	ctg	cgg	agc	ctt	672
Leu	Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Ala	Gly	Leu	Arg	Ser	Leu	
	210					215					220					
cag	gga	aag	gcc	gag	ctg	cgc	cgc	ctg	ctg	acc	aag	gtg	ctg	cag	gag	720
Gln	Gly	Lys	Ala	Glu	Leu	Arg	Arg	Leu	Leu	Thr	Lys	Val	Leu	Gln	Glu	
225					230					235					240	
agg	gat	ggc	ttg	cgg	aga	gtg	cac	agg	ccg	gca	gtc	ctg	gtg	aag	atc	768
Arg	Asp	Gly	Leu	Arg	Arg	Val	His	Arg	Pro	Ala	Val	Leu	Val	Lys	Ile	
				245					250					255		
gct	cct	gac	ctc	acc	agc	cag	gat	aag	gag	gac	att	gcc	agt	gtg	gtc	816
Ala	Pro	Asp	Leu	Thr	Ser	Gln	Asp	Lys	Glu	Asp	Ile	Ala	Ser	Val	Val	
			260					265					270			
aaa	gag	ttg	ggc	atc	gat	ggg	ctg	att	gtt	acg	aac	acc	acc	gtg	agt	864
Lys	Glu	Leu	Gly	Ile	Asp	Gly	Leu	Ile	Val	Thr	Asn	Thr	Thr	Val	Ser	
	275						280					285				
cgc	cct	gcg	ggc	ctc	cag	ggt	gcc	ctg	cgc	tct	gaa	aca	gga	ggg	ctg	912
Arg	Pro	Ala	Gly	Leu	Gln	Gly	Ala	Leu	Arg	Ser	Glu	Thr	Gly	Gly	Leu	
	290					295					300					
agt	ggg	aag	ccc	ctc	cgg	gat	tta	tca	act	caa	acc	att	cgg	gag	atg	960
Ser	Gly	Lys	Pro	Leu	Arg	Asp	Leu	Ser	Thr	Gln	Thr	Ile	Arg	Glu	Met	
305					310					315					320	
tat	gca	ctc	acc	caa	ggc	cga	gtt	ccc	ata	att	ggg	gtt	ggt	ggt	gtg	1008
Tyr	Ala	Leu	Thr	Gln	Gly	Arg	Val	Pro	Ile	Ile	Gly	Val	Gly	Gly	Val	
				325					330					335		
agc	agc	ggg	cag	gac	gcg	ctg	gag	aag	atc	cgg	gca	ggg	gcc	tcc	ctg	1056
Ser	Ser	Gly	Gln	Asp	Ala	Leu	Glu	Lys	Ile	Arg	Ala	Gly	Ala	Ser	Leu	
			340					345					350			
gtg	cag	ctg	tac	acg	gcc	ctc	acc	ttc	tgg	ggg	cca	ccc	gtt	gtg	ggc	1104
Val	Gln	Leu	Tyr	Thr	Ala	Leu	Thr	Phe	Trp	Gly	Pro	Pro	Val	Val	Gly	
	355						360					365				
aaa	gtc	aag	cgg	gaa	ctg	gag	gcc	ctt	ctg	aaa	gag	cag	ggc	ttt	ggc	1152
Lys	Val	Lys	Arg	Glu	Leu	Glu	Ala	Leu	Leu	Lys	Glu	Gln	Gly	Phe	Gly	
	370					375					380					
gga	gtc	aca	gat	gcc	att	gga	gca	gat	cat	cgg	agg	tgaggacagc				1198
Gly	Val	Thr	Asp	Ala	Ile	Gly	Ala	Asp	His	Arg	Arg					
385					390					395						
gtctgacggg	aagcctgata	tggaaccttc	ccaaggactc	aggcaagcct	ttgtggctgg											1258
atcatgagag	gagggactcc	atcttgagcc	atgtccccc	gcctggcatg	cgtgcactgt											1318
aaacgccaat	cggggggtca	ccaggatcaa	ccgcaggctt	tcttcagtc	cttggtcaga											1378
ccataaaactg	catttttgat	tctttgtgga	ttcaaaccct	aggatccatc	agtcttgcaa											1438
ggacattgaa	tattaggagg	aaaaagtc	ggaaaaaata	aagccattta	gaacctgg											1496

<210> 20
 <211> 396
 <212> PRT
 <213> Homo Sapien

<400> 20

Lys Leu Pro Trp Arg His Leu Gln Lys Arg Ala Gln Asp Ala Val Ile
 1 5 10 15
 Ile Leu Gly Gly Gly Leu Leu Phe Ala Ser Tyr Leu Met Ala Thr
 20 25 30
 Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr Leu Gln Gly
 35 40 45
 Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg Phe Thr Ser
 50 55 60
 Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp Met Leu Glu
 65 70 75 80
 Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly Ile Ala Ala
 85 90 95
 Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr Lys Met Gly
 100 105 110
 Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro Gln Glu Gly
 115 120 125
 Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln Ala Val Ile
 130 135 140
 Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val Glu His Arg
 145 150 155 160
 Leu Arg Ala Arg Gln Lys Gln Ala Lys Leu Thr Glu Asp Gly Leu
 165 170 175
 Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val Asp Ala Ala
 180 185 190
 Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu Ala Asp Tyr
 195 200 205
 Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu Arg Ser Leu
 210 215 220
 Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val Leu Gln Glu
 225 230 235 240
 Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu Val Lys Ile
 245 250 255
 Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala Ser Val Val
 260 265 270
 Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr Thr Val Ser
 275 280 285
 Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr Gly Gly Leu
 290 295 300
 Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile Arg Glu Met
 305 310 315 320
 Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val Gly Gly Val
 325 330 335
 Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly Ala Ser Leu
 340 345 350
 Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro Val Val Gly
 355 360 365
 Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln Gly Phe Gly
 370 375 380
 Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg
 385 390 395

<210> 21
 <211> 1101
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (1) ... (1101)
 <223> DHODH Truncated 39 kDa Construct

<300>

<301> Copeland, R.A., et al.
 <302> Recombinant Human Dihydroorotate Dehydrogenase
 <303> Arch. Biochem. Biophys. (1995)
 <304> 323
 <306> 79-86

<400> 21
 atg gcc acg gga gat gag cgt ttc tat gct gaa cac ctg atg ccg act 48
 Met Ala Thr Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr
 1 5 10 15
 ctg cag ggg ctg ctg gac ccg gag tca gcc cac aga ctg gct gtt cgc 96
 Leu Gln Gly Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg
 20 25 30
 ttc acc tcc ctg ggg ctc ctt cca cgg gcc aga ttt caa gac tct gac 144
 Phe Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp
 35 40 45
 atg ctg gaa gtg aga gtt ctg ggc cat aaa ttc cga aat cca gta gga 192
 Met Leu Glu Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly
 50 55 60
 att gct gca gga ttt gac aag cat ggg gaa gcc gtg gac gga ctt tat 240
 Ile Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr
 65 70 75 80
 aag atg ggc ttt ggt ttt gtt gag ata gga agt gtg act cca aaa cct 288
 Lys Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro
 85 90 95
 cag gaa gga aac cct aga ccc aga gtc ttc cgc ctc cct gag gac caa 336
 Gln Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln
 100 105 110
 gct gtc att aac agg tat gga ttt aac agt cac ggg ctt tca gtg gtg 384
 Ala Val Ile Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val
 115 120 125
 gaa cac agg tta cgg gcc aga cag cag aag cag gcc aag ctc aca gaa 432
 Glu His Arg Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu
 130 135 140
 gat gga ctg cct ctg ggg gtc aac ttg ggg aag aac aag acc tca gtg 480
 Asp Gly Leu Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val
 145 150 155 160
 gac gcc gcg gag gac tac gca gaa ggg gtg cgc gta ctg ggc ccc ctg 528
 Asp Ala Ala Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu
 165 170 175
 gcc gac tac ctg gtg gtg aat gtg tcc agc ccc aac act gcc ggg ctg 576
 Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu
 180 185 190
 cgg agc ctt cag gga aag gcc gag ctg cgc cgc ctg ctg acc aag gtg 624
 Arg Ser Leu Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val
 195 200 205
 ctg cag gag agg gat ggc ttg cgg aga gtg cac agg ccg gca gtc ctg 672
 Leu Gln Glu Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu
 210 215 220

gtg aag atc gct cct gac ctc acc agc cag gat aag gag gac att gcc	720
Val Lys Ile Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala	
225 230 235 240	
agt gtg gtc aaa gag ttg ggc atc gat ggg ctg att gtt acg aac acc	768
Ser Val Val Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr	
245 250 255	
acc gtg agt cgc cct gcg ggc ctc cag ggt gcc ctg cgc tct gaa aca	816
Thr Val Ser Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr	
260 265 270	
gga ggg ctg agt ggg aag ccc ctc cgg gat tta tca act caa acc att	864
Gly Gly Leu Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile	
275 280 285	
cgg gag atg tat gca ctc acc caa ggc cga gtt ccc ata att ggg gtt	912
Arg Glu Met Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val	
290 295 300	
ggt ggt gtg agc agc ggg cag gac gcg ctg gag aag atc cgg gca ggg	960
Gly Gly Val Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly	
305 310 315 320	
gcc tcc ctg gtg cag ctg tac acg gcc ctc acc ttc tgg ggg cca ccc	1008
Ala Ser Leu Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro	
325 330 335	
gtt gtg ggc aaa gtc aag cgg gaa ctg gag gcc ctt ctg aaa gag cag	1056
Val Val Gly Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln	
340 345 350	
ggc ttt ggc gga gtc aca gat gcc att gga gca gat cat cgg agg	1101
Gly Phe Gly Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg	
355 360 365	

<210> 22
 <211> 367
 <212> PRT
 <213> Homo sapien

<400> 22
 Met Ala Thr Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr
 1 5 10 15
 Leu Gln Gly Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg
 20 25 30
 Phe Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp
 35 40 45
 Met Leu Glu Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly
 50 55 60
 Ile Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr
 65 70 75 80
 Lys Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro
 85 90 95
 Gln Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln
 100 105 110
 Ala Val Ile Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val
 115 120 125
 Glu His Arg Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu
 130 135 140

```

Asp Gly Leu Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val
145      150      155      160
Asp Ala Ala Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu
      165      170      175
Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu
      180      185      190
Arg Ser Leu Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val
      195      200      205
Leu Gln Glu Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu
      210      215      220
Val Lys Ile Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala
225      230      235      240
Ser Val Val Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr
      245      250      255
Thr Val Ser Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr
      260      265      270
Gly Gly Leu Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile
      275      280      285
Arg Glu Met Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val
      290      295      300
Gly Gly Val Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly
305      310      315      320
Ala Ser Leu Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro
      325      330      335
Val Val Gly Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln
      340      345      350
Gly Phe Gly Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg
      355      360      365

```

```

<210> 23
<211> 1101
<212> DNA
<213> Homo sapien

```

```

<220>
<221> mutation
<222> 79
<223> C to G mutation

```

```

<221> mutation
<222> 80
<223> A to C mutation

```

```

<221> CDS
<222> (4)...(1101)
<223> His26Ala DHODH mutant

```

```

<300>
<301> Davis et al.
<302> Histidine to Alanine mutants of Human Dihydroorota
<303> Biochem. Pharmacol. (1997)
<304> 54
<306> 459-465

```

```

<400> 23
atg gcc acg gga gat gag cgt ttc tat gct gaa cac ctg atg ccg act      48
  Ala Thr Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr
    1              5              10              15

ctg cag ggg ctg ctg gac ccg gag tca gcc gcc aga ctg gct gtt cgc      96
Leu Gln Gly Leu Leu Asp Pro Glu Ser Ala Ala Arg Leu Ala Val Arg
      20              25              30

```

ttc acc tcc ctg ggg ctc ctt cca cgg gcc aga ttt caa gac tct gac	144
Phe Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp	
35 40 45	
atg ctg gaa gtg aga gtt ctg ggc cat aaa ttc cga aat cca gta gga	192
Met Leu Glu Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly	
50 55 60	
att gct gca gga ttt gac aag cat ggg gaa gcc gtg gac gga ctt tat	240
Ile Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr	
65 70 75	
aag atg ggc ttt ggt ttt gtt gag ata gga agt gtg act cca aaa cct	288
Lys Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro	
80 85 90 95	
cag gaa gga aac cct aga ccc aga gtc ttc cgc ctc cct gag gac caa	336
Gln Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln	
100 105 110	
gct gtc att aac agg tat gga ttt aac agt cac ggg ctt tca gtg gtg	384
Ala Val Ile Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val	
115 120 125	
gaa cac agg tta cgg gcc aga cag cag aag cag gcc aag ctc aca gaa	432
Glu His Arg Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu	
130 135 140	
gat gga ctg cct ctg ggg gtc aac ttg ggg aag aac aag acc tca gtg	480
Asp Gly Leu Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val	
145 150 155	
gac gcc gcg gag gac tac gca gaa ggg gtg cgc gta ctg ggc ccc ctg	528
Asp Ala Ala Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu	
160 165 170 175	
gcc gac tac ctg gtg gtg aat gtg tcc agc ccc aac act gcc ggg ctg	576
Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu	
180 185 190	
cgg agc ctt cag gga aag gcc gag ctg cgc cgc ctg ctg acc aag gtg	624
Arg Ser Leu Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val	
195 200 205	
ctg cag gag agg gat ggc ttg cgg aga gtg cac agg ccg gca gtc ctg	672
Leu Gln Glu Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu	
210 215 220	
gtg aag atc gct cct gac ctc acc agc cag gat aag gag gac att gcc	720
Val Lys Ile Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala	
225 230 235	
agt gtg gtc aaa gag ttg ggc atc gat ggg ctg att gtt acg aac acc	768
Ser Val Val Lys Glu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr	
240 245 250 255	
acc gtg agt cgc cct gcg ggc ctc cag ggt gcc ctg cgc tct gaa aca	816
Thr Val Ser Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr	
260 265 270	
gga ggg ctg agt ggg aag ccc ctc cgg gat tta tca act caa acc att	864

Gly	Gly	Leu	Ser	Gly	Lys	Pro	Leu	Arg	Asp	Leu	Ser	Thr	Gln	Thr	Ile		
			275					280					285				
cgg	gag	atg	tat	gca	ctc	acc	caa	ggc	cga	gtt	ccc	ata	att	ggg	gtt	912	
Arg	Glu	Met	Tyr	Ala	Leu	Thr	Gln	Gly	Arg	Val	Pro	Ile	Ile	Gly	Val		
		290					295				300						
ggt	ggt	gtg	agc	agc	ggg	cag	gac	gcg	ctg	gag	aag	atc	cgg	gca	ggg	960	
Gly	Gly	Val	Ser	Ser	Gly	Gln	Asp	Ala	Leu	Glu	Lys	Ile	Arg	Ala	Gly		
	305					310					315						
gcc	tcc	ctg	gtg	cag	ctg	tac	acg	gcc	ctc	acc	ttc	tgg	ggg	cca	ccc	1008	
Ala	Ser	Leu	Val	Gln		Tyr	Thr	Ala	Leu	Thr	Phe	Trp	Gly	Pro	Pro		
					325					330					335		
gtt	gtg	ggc	aaa	gtc	aag	cgg	gaa	ctg	gag	gcc	ctt	ctg	aaa	gag	cag	1056	
Val	Val	Gly	Lys	Val	Lys	Arg	Glu	Leu	Glu	Ala	Leu	Leu	Lys	Glu	Gln		
				340				345						350			
ggc	ttt	ggc	gga	gtc	aca	gat	gcc	att	gga	gca	gat	cat	cgg	agg		1101	
Gly	Phe	Gly	Gly	Val	Thr	Asp	Ala	Ile	Gly	Ala	Asp	His	Arg	Arg			
			355					360					365				

<210> 24
 <211> 366
 <212> PRT
 <213> Homo sapien

<400> 24

Ala	Thr	Gly	Asp	Glu	Arg	Phe	Tyr	Ala	Glu	His	Leu	Met	Pro	Thr	Leu		
1				5					10					15			
Gln	Gly	Leu	Leu	Asp	Pro	Glu	Ser	Ala	Ala	Arg	Leu	Ala	Val	Arg	Phe		
		20						25					30				
Thr	Ser	Leu	Gly	Leu	Leu	Pro	Arg	Ala	Arg	Phe	Gln	Asp	Ser	Asp	Met		
		35					40					45					
Leu	Glu	Val	Arg	Val	Leu	Gly	His	Lys	Phe	Arg	Asn	Pro	Val	Gly	Ile		
	50					55					60						
Ala	Ala	Gly	Phe	Asp	Lys	His	Gly	Glu	Ala	Val	Asp	Gly	Leu	Tyr	Lys		
65					70				75					80			
Met	Gly	Phe	Gly	Phe	Val	Glu	Ile	Gly	Ser	Val	Thr	Pro	Lys	Pro	Gln		
			85					90					95				
Glu	Gly	Asn	Pro	Arg	Pro	Arg	Val	Phe	Arg	Leu	Pro	Glu	Asp	Gln	Ala		
		100						105					110				
Val	Ile	Asn	Arg	Tyr	Gly	Phe	Asn	Ser	His	Gly	Leu	Ser	Val	Val	Glu		
		115					120					125					
His	Arg	Leu	Arg	Ala	Arg	Gln	Gln	Lys	Gln	Ala	Lys	Leu	Thr	Glu	Asp		
	130					135					140						
Gly	Leu	Pro	Leu	Gly	Val	Asn	Leu	Gly	Lys	Asn	Lys	Thr	Ser	Val	Asp		
145					150				155						160		
Ala	Ala	Glu	Asp	Tyr	Ala	Glu	Gly	Val	Arg	Val	Leu	Gly	Pro	Leu	Ala		
			165					170						175			
Asp	Tyr	Leu	Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Ala	Gly	Leu	Arg		
		180					185						190				
Ser	Leu	Gln	Gly	Lys	Ala	Glu	Leu	Arg	Arg	Leu	Leu	Thr	Lys	Val	Leu		
	195						200					205					
Gln	Glu	Arg	Asp	Gly	Leu	Arg	Arg	Val	His	Arg	Pro	Ala	Val	Leu	Val		
	210					215					220						
Lys	Ile	Ala	Pro	Asp	Leu	Thr	Ser	Gln	Asp	Lys	Glu	Asp	Ile	Ala	Ser		
225					230				235						240		
Val	Val	Lys	Glu	Leu	Gly	Ile	Asp	Gly	Leu	Ile	Val	Thr	Asn	Thr	Thr		
				245					250					255			

Val Ser Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr Gly
 260 265 270
 Gly Leu Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile Arg
 275 280 285
 Glu Met Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val Gly
 290 295 300
 Gly Val Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly Ala
 305 310 315 320
 Ser Leu Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro Val
 325 330 335
 Val Gly Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln Gly
 340 345 350
 Phe Gly Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg
 355 360 365

<210> 25
 <211> 1560
 <212> DNA
 <213> Aspergillus nidulans

<220>
 <221> CDS
 <222> (1)...(1560)
 <223> Aspergillus nidulans Val200Glu mutant DHODH cDNA

<221> mutation
 <222> 599
 <223> T to A mutataation

<400> 25
 atg gct acg aat tct ttc cga aaa ctc act ttt tca gga gcc tcc cgt 48
 Met Ala Thr Asn Ser Phe Arg Lys Leu Thr Phe Ser Gly Ala Ser Arg
 1 5 10 15
 ctg ggt ggt tgt cgc cgt ctc cca cta acc tgc aga caa ctt cga ttc 96
 Leu Gly Gly Cys Arg Arg Leu Pro Leu Thr Cys Arg Gln Leu Arg Phe
 20 25 30
 gcc tcc gac agc gga gcc gca gcg gca act aca aaa gca acg gcc gaa 144
 Ala Ser Asp Ser Gly Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu
 35 40 45
 tca gca gcc gag tca gct agt ata aac gtc aaa gag gca ccc aaa aag 192
 Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys
 50 55 60
 gcc gga cgg ggc ctg cgg cgc acg gtc ctg gga acg tcg ttg gcg ctg 240
 Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu
 65 70 75 80
 acg ctg ctg gtt gga tat gtc tac ggg acg gac acc cgg gcg agt gtg 288
 Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val
 85 90 95
 cat cgg tac ggt gtt gtg ccg ctg att aga gca ttg tat cct gat gcg 336
 His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala
 100 105 110
 gaa gat gcg cat cat att ggt gtc gat act tta aag atg ctg tat aag 384
 Glu Asp Ala His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys
 115 120 125

tat ggt ctg cat cca agg gaa cgg ggg gat ccg gat gga gat ggg gcg Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala 130 135 140	432
ctg gcg aca gag gtc ttt ggg tat aca ctg tca aac cca att ggc ata Leu Ala Thr Glu Val Phe Gly Tyr Thr Leu Ser Asn Pro Ile Gly Ile 145 150 155 160	480
tcg ggc ggc ctg gac aag cat gct gag atc cct gat ccg ctg ttc gcg Ser Gly Gly Leu Asp Lys His Ala Glu Ile Pro Asp Pro Leu Phe Ala 165 170 175	528
atc ggt cct gcc att gtc gaa gtc ggg ggt acg aca ccc tta cca cag Ile Gly Pro Ala Ile Val Glu Val Gly Gly Thr Thr Pro Leu Pro Gln 180 185 190	576
gat ggt aac ccg cgt cct cgc gaa ttc cga ctt cca tca cag aga gcg Asp Gly Asn Pro Arg Pro Arg Glu Phe Arg Leu Pro Ser Gln Arg Ala 195 200 205	624
atg ata aac cgg tac ggc ctc aac tcc aaa ggc gca gat cac atg gca Met Ile Asn Arg Tyr Gly Leu Asn Ser Lys Gly Ala Asp His Met Ala 210 215 220	672
gct atc ttg gag caa cga gta cgc gat ttt gcc tac gca aac gga ttt Ala Ile Leu Glu Gln Arg Val Arg Asp Phe Ala Tyr Ala Asn Gly Phe 225 230 235 240	720
ggg gca tac gat gcg gct aag cag cgt gta ttg gac ggc gaa gct ggt Gly Ala Tyr Asp Ala Ala Lys Gln Arg Val Leu Asp Gly Glu Ala Gly 245 250 255	768
gtg cca cca ggt agt ctt cag cct ggt aag ctt tta gct gtc caa gtg Val Pro Pro Gly Ser Leu Gln Pro Gly Lys Leu Leu Ala Val Gln Val 260 265 270	816
gca aag aac aag gcc act cct gac ggc gac att gaa gcc atc aag cgc Ala Lys Asn Lys Ala Thr Pro Asp Gly Asp Ile Glu Ala Ile Lys Arg 275 280 285	864
gac tat gtg tat tgc gtg gac cgt gtg gcc aaa tac gct gat att ctt Asp Tyr Val Tyr Cys Val Asp Arg Val Ala Lys Tyr Ala Asp Ile Leu 290 295 300	912
gtt gtg aat gta tcg agc ccc aac aca ccc ggt ctc cgt gac ctt caa Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly Leu Arg Asp Leu Gln 305 310 315 320	960
gcc act gcc ccg ctc aca gct atc ttg agt gct gtc gtt ggc gcg gca Ala Thr Ala Pro Leu Thr Ala Ile Leu Ser Ala Val Val Gly Ala Ala 325 330 335	1008
aag agc gtg aac cgc aag acc aaa cca tat gtt atg gtc aag gtc agt Lys Ser Val Asn Arg Lys Thr Lys Pro Tyr Val Met Val Lys Val Ser 340 345 350	1056
ccg gat gaa gac tca gat gaa caa gtc tct ggt atc tgc gac gcc gtc Pro Asp Glu Asp Ser Asp Glu Gln Val Ser Gly Ile Cys Asp Ala Val 355 360 365	1104
cga gca tcc ggt gtc gac gga gtg att gtc gga aac aca aca aac cgt Arg Ala Ser Gly Val Asp Gly Val Ile Val Gly Asn Thr Thr Asn Arg	1152

370	375	380	
cgc ccc gac cct ata ccc caa ggt tac act ctt ccg gcc aag gag cag Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln 385 390 395 400			1200
gca acg ttg aaa gaa acc ggc ggg tat tca ggt cca cag ctg ttc gat Ala Thr Leu Lys Glu Thr Gly Gly Tyr Ser Gly Pro Gln Leu Phe Asp 405 410 415			1248
cgc aca gtg gcc ctt gtg gct cgg tac cgc tcc atg ctg gat gcg gag Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Ala Glu 420 425 430			1296
tcg gaa acg gcc gga tcc gcc aag gat tca gca gcg acc ata gcg caa Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln 435 440 445			1344
aca gag cca ggc tcg gaa aac gtt cct cct gtg gaa gcg cca agc gga Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly 450 455 460			1392
ctg ccg cgc aaa gtt atc ttc gct tcg ggt ggt atc acc aac ggg aag Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys 465 470 475 480			1440
cag gct cac gct gtt tta gac aca ggg gca tct gtt gcc atg atg tac Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr 485 490 495			1488
acc ggt gtg gtc tat ggt ggc gtc ggc act gtc act cga gtg aag caa Thr Gly Val Val Tyr Gly Gly Val Gly Thr Val Thr Arg Val Lys Gln 500 505 510			1536
gaa ctt cga acg gcg aaa aag gag Glu Leu Arg Thr Ala Lys Lys Glu 515 520			1560

<210> 26
 <211> 520
 <212> PRT
 <213> Aspergillus nidulans

<400> 26
 Met Ala Thr Asn Ser Phe Arg Lys Leu Thr Phe Ser Gly Ala Ser Arg
 1 5 10 15
 Leu Gly Gly Cys Arg Arg Leu Pro Leu Thr Cys Arg Gln Leu Arg Phe
 20 25 30
 Ala Ser Asp Ser Gly Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu
 35 40 45
 Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys
 50 55 60
 Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu
 65 70 75 80
 Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val
 85 90 95
 His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala
 100 105 110
 Glu Asp Ala His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys
 115 120 125
 Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala

130	135	140
Leu Ala Thr Glu Val	Phe Gly Tyr Thr	Leu Ser Asn Pro Ile Gly Ile
145	150	155
Ser Gly Gly Leu Asp	Lys His Ala Glu	Ile Pro Asp Pro Leu Phe Ala
165	170	175
Ile Gly Pro Ala Ile	Val Glu Val Gly	Gly Thr Thr Pro Leu Pro Gln
180	185	190
Asp Gly Asn Pro Arg	Pro Arg Glu Phe	Arg Leu Pro Ser Gln Arg Ala
195	200	205
Met Ile Asn Arg Tyr	Gly Leu Asn Ser	Lys Gly Ala Asp His Met Ala
210	215	220
Ala Ile Leu Glu Gln	Arg Val Arg Asp	Phe Ala Tyr Ala Asn Gly Phe
225	230	235
Gly Ala Tyr Asp Ala	Ala Lys Gln Arg	Val Leu Asp Gly Glu Ala Gly
245	250	255
Val Pro Pro Gly Ser	Leu Gln Pro Gly	Lys Leu Leu Ala Val Gln Val
260	265	270
Ala Lys Asn Lys Ala	Thr Pro Asp Gly	Asp Ile Glu Ala Ile Lys Arg
275	280	285
Asp Tyr Val Tyr Cys	Val Asp Arg Val	Ala Lys Tyr Ala Asp Ile Leu
290	295	300
Val Val Asn Val Ser	Ser Pro Asn Thr	Pro Gly Leu Arg Asp Leu Gln
305	310	315
Ala Thr Ala Pro Leu	Thr Ala Ile Leu	Ser Ala Val Val Gly Ala Ala
325	330	335
Lys Ser Val Asn Arg	Lys Thr Lys Pro	Tyr Val Met Val Lys Val Ser
340	345	350
Pro Asp Glu Asp Ser	Asp Glu Gln Val	Ser Gly Ile Cys Asp Ala Val
355	360	365
Arg Ala Ser Gly Val	Asp Gly Val Ile	Val Gly Asn Thr Thr Asn Arg
370	375	380
Arg Pro Asp Pro Ile	Pro Gln Gly Tyr	Thr Leu Pro Ala Lys Glu Gln
385	390	395
Ala Thr Leu Lys Glu	Thr Gly Gly Tyr	Ser Gly Pro Gln Leu Phe Asp
405	410	415
Arg Thr Val Ala Leu	Val Ala Arg Tyr	Arg Ser Met Leu Asp Ala Glu
420	425	430
Ser Glu Thr Ala Gly	Ser Ala Lys Asp	Ser Ala Ala Thr Ile Ala Gln
435	440	445
Thr Glu Pro Gly Ser	Glu Asn Val Pro	Pro Val Glu Ala Pro Ser Gly
450	455	460
Leu Pro Arg Lys Val	Ile Phe Ala Ser	Gly Gly Ile Thr Asn Gly Lys
465	470	475
Gln Ala His Ala Val	Leu Asp Thr Gly	Ala Ser Val Ala Met Met Tyr
485	490	495
Thr Gly Val Val Tyr	Gly Gly Val Gly	Thr Val Thr Arg Val Lys Gln
500	505	510
Glu Leu Arg Thr Ala	Lys Lys Glu	
515	520	

<210> 27

<211> 1560

<212> DNA

<213> Aspergillus nidulans

<220>

<221> CDS

<222> (1)...(1560)

<223> Aspergillus nidulans Ala115Val mutant DHODH cDNA

<221> mutation

<222> 344

<223> C to T mutation

<400> 27

atg gct acg aat tct ttc cga aaa ctc act ttt tca gga gcc tcc cgt	48
Met Ala Thr Asn Ser Phe Arg Lys Leu Thr Phe Ser Gly Ala Ser Arg	
1 5 10 15	
ctg ggt ggt tgt cgc cgt ctc cca cta acc tgc aga caa ctt cga ttc	96
Leu Gly Gly Cys Arg Arg Leu Pro Leu Thr Cys Arg Gln Leu Arg Phe	
20 25 30	
gcc tcc gac agc gga gcc gca gcg gca act aca aaa gca acg gcc gaa	144
Ala Ser Asp Ser Gly Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu	
35 40 45	
tca gca gcc gag tca gct agt ata aac gtc aaa gag gca ccc aaa aag	192
Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys	
50 55 60	
gcc gga cgg ggc ctg cgg cgc acg gtc ctg gga acg tcg ttg gcg ctg	240
Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu	
65 70 75 80	
acg ctg ctg gtt gga tat gtc tac ggg acg gac acc cgg gcg agt gtg	288
Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val	
85 90 95	
cat cgg tac ggt gtt gtg ccg ctg att aga gca ttg tat cct gat gcg	336
His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala	
100 105 110	
gaa gat gtg cat cat att ggt gtc gat act tta aag atg ctg tat aag	384
Glu Asp Val His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys	
115 120 125	
tat ggt ctg cat cca agg gaa cgg ggg gat ccg gat gga gat ggg gcg	432
Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala	
130 135 140	
ctg gcg aca gag gtc ttt ggg tat aca ctg tca aac cca att ggc ata	480
Leu Ala Thr Glu Val Phe Gly Tyr Thr Leu Ser Asn Pro Ile Gly Ile	
145 150 155 160	
tcg ggc ggc ctg gac aag cat gct gag atc cct gat ccg ctg ttc gcg	528
Ser Gly Gly Leu Asp Lys His Ala Glu Ile Pro Asp Pro Leu Phe Ala	
165 170 175	
atc ggt cct gcc att gtc gaa gtc ggg ggt acg aca ccc tta cca cag	576
Ile Gly Pro Ala Ile Val Glu Val Gly Gly Thr Thr Pro Leu Pro Gln	
180 185 190	
gat ggt aac ccg cgt cct cgc gta ttc cga ctt cca tca cag aga gcg	624
Asp Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Ser Gln Arg Ala	
195 200 205	
atg ata aac cgg tac ggc ctc aac tcc aaa ggc gca gat cac atg gca	672
Met Ile Asn Arg Tyr Gly Leu Asn Ser Lys Gly Ala Asp His Met Ala	
210 215 220	
gct atc ttg gag caa cga gta cgc gat ttt gcc tac gca aac gga ttt	720
Ala Ile Leu Glu Gln Arg Val Arg Asp Phe Ala Tyr Ala Asn Gly Phe	
225 230 235 240	

ggg gca tac gat gcg gct aag cag cgt gta ttg gac ggc gaa gct ggt	768
Gly Ala Tyr Asp Ala Ala Lys Gln Arg Val Leu Asp Gly Glu Ala Gly	
245 250 255	
gtg cca cca ggt agt ctt cag cct ggt aag ctt tta gct gtc caa gtg	816
Val Pro Pro Gly Ser Leu Gln Pro Gly Lys Leu Leu Ala Val Gln Val	
260 265 270	
gca aag aac aag gcc act cct gac ggc gac att gaa gcc atc aag cgc	864
Ala Lys Asn Lys Ala Thr Pro Asp Gly Asp Ile Glu Ala Ile Lys Arg	
275 280 285	
gac tat gtg tat tgc gtg gac cgt gtg gcc aaa tac gct gat att ctt	912
Asp Tyr Val Tyr Cys Val Asp Arg Val Ala Lys Tyr Ala Asp Ile Leu	
290 295 300	
gtt gtg aat gta tgc agc ccc aac aca ccc ggt ctc cgt gac ctt caa	960
Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly Leu Arg Asp Leu Gln	
305 310 315 320	
gcc act gcc ccg ctc aca gct atc ttg agt gct gtc gtt ggc gcg gca	1008
Ala Thr Ala Pro Leu Thr Ala Ile Leu Ser Ala Val Val Gly Ala Ala	
325 330 335	
aag agc gtg aac cgc aag acc aaa cca tat gtt atg gtc aag gtc agt	1056
Lys Ser Val Asn Arg Lys Thr Lys Pro Tyr Val Met Val Lys Val Ser	
340 345 350	
ccg gat gaa gac tca gat gaa caa gtc tct ggt atc tgc gac gcc gtc	1104
Pro Asp Glu Asp Ser Asp Glu Gln Val Ser Gly Ile Cys Asp Ala Val	
355 360 365	
cga gca tcc ggt gtc gac gga gtg att gtc gga aac aca aca aac cgt	1152
Arg Ala Ser Gly Val Asp Gly Val Ile Val Gly Asn Thr Thr Asn Arg	
370 375 380	
cgc ccc gac cct ata ccc caa ggt tac act ctt ccg gcc aag gag cag	1200
Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln	
385 390 395 400	
gca acg ttg aaa gaa acc ggc ggg tat tca ggt cca cag ctg ttc gat	1248
Ala Thr Leu Lys Glu Thr Gly Gly Tyr Ser Gly Pro Gln Leu Phe Asp	
405 410 415	
cgc aca gtg gcc ctt gtg gct cgg tac cgc tcc atg ctg gat gcg gag	1296
Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Asp Ala Glu	
420 425 430	
tcg gaa acg gcc gga tcc gcc aag gat tca gca gcg acc ata gcg caa	1344
Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln	
435 440 445	
aca gag cca ggc tcg gaa aac gtt cct cct gtg gaa gcg cca agc gga	1392
Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly	
450 455 460	
ctg ccg cgc aaa gtt atc ttc gct tcg ggt ggt atc acc aac ggg aag	1440
Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys	
465 470 475 480	
cag gct cac gct gtt tta gac aca ggg gca tct gtt gcc atg atg tac	1488

gaa ctt cga acg gcg aaa aag gag 1560
Glu Leu Arg Thr Ala Lys Lys Glu
515 520

```
<210> 28
<211> 520
<212> PRT
<213> Aspergillus nidulans
```

<400>	28														
Met	Ala	Thr	Asn	Ser	Phe	Arg	Lys	Leu	Thr	Phe	Ser	Gly	Ala	Ser	Arg
1				5					10					15	
Leu	Gly	Gly	Cys	Arg	Arg	Leu	Pro	Leu	Thr	Cys	Arg	Gln	Leu	Arg	Phe
			20					25					30		
Ala	Ser	Asp	Ser	Gly	Ala	Ala	Ala	Ala	Thr	Thr	Lys	Ala	Thr	Ala	Glu
		35				40						45			
Ser	Ala	Ala	Glu	Ser	Ala	Ser	Ile	Asn	Val	Lys	Glu	Ala	Pro	Lys	Lys
	50					55				60					
Ala	Gly	Arg	Gly	Leu	Arg	Arg	Thr	Val	Leu	Gly	Thr	Ser	Leu	Ala	Leu
65				70					75						80
Thr	Leu	Leu	Val	Gly	Tyr	Val	Tyr	Gly	Thr	Asp	Thr	Arg	Ala	Ser	Val
			85					90						95	
His	Arg	Tyr	Gly	Val	Val	Pro	Leu	Ile	Arg	Ala	Leu	Tyr	Pro	Asp	Ala
			100					105					110		
Glu	Asp	Val	His	His	Ile	Gly	Val	Asp	Thr	Leu	Lys	Met	Leu	Tyr	Lys
		115					120					125			
Tyr	Gly	Leu	His	Pro	Arg	Glu	Arg	Gly	Asp	Pro	Asp	Gly	Asp	Gly	Ala
	130					135					140				
Leu	Ala	Thr	Glu	Val	Phe	Gly	Tyr	Thr	Leu	Ser	Asn	Pro	Ile	Gly	Ile
145					150					155					160
Ser	Gly	Gly	Leu	Asp	Lys	His	Ala	Glu	Ile	Pro	Asp	Pro	Leu	Phe	Ala
				165					170					175	
Ile	Gly	Pro	Ala	Ile	Val	Glu	Val	Gly	Gly	Thr	Thr	Pro	Leu	Pro	Gln
			180					185					190		
Asp	Gly	Asn	Pro	Arg	Pro	Arg	Val	Phe	Arg	Leu	Pro	Ser	Gln	Arg	Ala
		195					200					205			
Met	Ile	Asn	Arg	Tyr	Gly	Leu	Asn	Ser	Lys	Gly	Ala	Asp	His	Met	Ala
	210				215						220				
Ala	Ile	Leu	Glu	Gln	Arg	Val	Arg	Asp	Phe	Ala	Tyr	Ala	Asn	Gly	Phe
225				230					235						240
Gly	Ala	Tyr	Asp	Ala	Ala	Lys	Gln	Arg	Val	Leu	Asp	Gly	Glu	Ala	Gly
			245						250				255		
Val	Pro	Pro	Gly	Ser	Leu	Gln	Pro	Gly	Lys	Leu	Leu	Ala	Val	Gln	Val
			260					265					270		
Ala	Lys	Asn	Lys	Ala	Thr	Pro	Asp	Gly	Asp	Ile	Glu	Ala	Ile	Lys	Arg
		275					280					285			
Asp	Tyr	Val	Tyr	Cys	Val	Asp	Arg	Val	Ala	Lys	Tyr	Ala	Asp	Ile	Leu
	290					295					300				
Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Pro	Gly	Leu	Arg	Asp	Leu	Gln
305				310						315					320
Ala	Thr	Ala	Pro	Leu	Thr	Ala	Ile	Leu	Ser	Ala	Val	Val	Gly	Ala	Ala
			325						330				335		
Lys	Ser	Val	Asn	Arg	Lys	Thr	Lys	Pro	Tyr	Val	Met	Val	Lys	Val	Ser
			340		</										

Pro Asp Glu Asp Ser Asp Glu Gln Val Ser Gly Ile Cys Asp Ala Val
 355 360 365
 Arg Ala Ser Gly Val Asp Gly Val Ile Val Gly Asn Thr Thr Asn Arg
 370 375 380
 Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln
 385 390 395 400
 Ala Thr Leu Lys Glu Thr Gly Gly Tyr Ser Gly Pro Gln Leu Phe Asp
 405 410 415
 Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Asp Ala Glu
 420 425 430
 Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln
 435 440 445
 Thr Glu Thr Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly
 450 455 460
 Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys
 465 470 475 480
 Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr
 485 490 495
 Thr Gly Val Val Tyr Gly Gly Val Gly Thr Val Thr Arg Val Lys Gln
 500 505 510
 Glu Leu Arg Thr Ala Lys Lys Glu
 515 520

<210> 29

<211> 1707

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (67)...(1611)

<223> wild-type IMP dehydrogenase cDNA

<400> 29

cctctgcggc gcggtcctcg ggcggcgcg gttctcggag ccacgcgtct gtcttcctcc 60
 gtggtc atg gcg gac tac ctg att agc gga ggc acc tct tac gtg ccg 108
 Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro
 1 5 10

gac gac ggg ctc aca gcg cag cag ctc ttc aac tgc ggg gac ggc ctc 156
 Asp Asp Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu
 15 20 25 30

acc tac aat gat ttt ctc att ctt cct ggg tat atc gac ttc act gca 204
 Thr Tyr Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala
 35 40 45

gat cag gtg gac ttg acg tct gct cta act aag aag att aca cta aag 252
 Asp Gln Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys
 50 55 60

acc cca ttg gtt tcc tca ccc atg gac act gtc aca gag gct gga atg 300
 Thr Pro Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met
 65 70 75

gcc atc gcg atg gcg ctt aca gga ggt att ggt ttc atc cac cac aac 348
 Ala Ile Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn
 80 85 90

tgc aca cct gaa ttc cag gcc aat gaa gtt cgg aaa gtg aag aaa tac 396
 Cys Thr Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr
 95 100 105 110

gaa cag gga ttc atc act gac ccc gtg gtc ctt agc ccc aag gat cgt	444
Glu Gln Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg	
115 120 125	
gta cgc gat gtt ttt gag gcc aaa gcc agg cat ggc ttc tgt ggt atc	492
Val Arg Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile	
130 135 140	
ccc atc aca gat aca ggc cgg atg ggg agt cga ttg gtg ggc atc atc	540
Pro Ile Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile	
145 150 155	
tcc tca agg gac att gat ttc ctc aag gag gaa gag cat gac cgg ttc	588
Ser Ser Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Arg Phe	
160 165 170	
ttg gaa gag atc atg act aag agg gaa gat ttg gtg gtc gcc cct gcc	636
Leu Glu Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Ala	
175 180 185 190	
ggc gtc act ctg aaa gag gca aat gag att ctg cag cga agt aaa aag	684
Gly Val Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys	
195 200 205	
gga aag ttg ccc att gtg aat gaa aat gat gag ctg gta gcc atc att	732
Gly Lys Leu Pro Ile Val Asn Glu Asn Asp Glu Leu Val Ala Ile Ile	
210 215 220	
gcc cgg aca gac cta aag aag aat cgt gat tac ccc ctg gcc tcc aaa	780
Ala Arg Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys	
225 230 235	
gat gcc aag aag caa ctg ctg tgt ggg gca gcc att ggc act cat gag	828
Asp Ala Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu	
240 245 250	
gat gac aag tat agg ctg gac tta ctg gcc ctt gct ggt gtg gat gta	876
Asp Asp Lys Tyr Arg Leu Asp Leu Leu Ala Leu Ala Gly Val Asp Val	
255 260 265 270	
gtg gtt ttg gac tct tcc cag gga aac tcc atc ttc caa atc aat atg	924
Val Val Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met	
275 280 285	
atc aaa tac atc aag gag aag tat ccc agt cta cag gtc att gga ggc	972
Ile Lys Tyr Ile Lys Glu Lys Tyr Pro Ser Leu Gln Val Ile Gly Gly	
290 295 300	
aat gta gtc act gct gcg caa gcc aag aac ctc ata gat gca ggt gta	1020
Asn Val Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val	
305 310 315	
gat gct ttg cga gtc ggc atg gga agt ggt tcc atc tgc atc acc cag	1068
Asp Ala Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln	
320 325 330	
gaa gtg ttg gcc tgt ggg cgg ccc caa gcc aca gca gtg tac aag gtc	1116
Glu Val Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val	
335 340 345 350	
tct gag tat gcc cgt cgc ttt ggt gtt cct gtt att gct gat gga gga	1164

```

Ser Glu Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly
      355      360      365
atc caa aat gtg ggt cat att gcc aaa gct ttg gct ctt ggg gct tcc 1212
Ile Gln Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser
      370      375      380
aca gtc atg atg ggc tcc ctc ctg gct gcc acc act gag gcc cct ggc 1260
Thr Val Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly
      385      390      395
gag tac ttc ttc tca gat ggg atc cgg ctg aag aaa tac cga ggt atg 1308
Glu Tyr Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met
      400      405      410
ggg tct ctt gat gcc atg gac aaa cat ctc agc agc cag aac cga tac 1356
Gly Ser Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr
      415      420      425
ttc agt gaa gct gac aaa atc aaa gtg gcc caa gga gtt tca ggg gca 1404
Phe Ser Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala
      435      440      445
gtg cag gac aag ggg tct atc cac aag ttc gtt cct tac ctg att gct 1452
Val Gln Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala
      450      455      460
ggc atc cag cat tcc tgt caa gac att ggt gcc aag agt tta acc caa 1500
Gly Ile Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln
      465      470      475
gtc aga gcc atg acg tac tcg ggg gag ctt aaa ttt gag aag agg aca 1548
Val Arg Ala Met Thr Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr
      480      485      490
tcc tct gct cag gtg gaa ggt ggc gtc cac agc ctc cat tcg tac gag 1596
Ser Ser Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu
      495      500      505      510
aaa cgg ctt ttc tga aaacagatcc agtatatgcc ttgaattttt caataaaagt 1651
Lys Arg Leu Phe *

```

```

ttgggaaaaa aaaagtgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1707

```

```

<210> 30
<211> 514
<212> PRT
<213> Mus musculus

```

```

<400> 30
Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
 1      5      10
Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
      20      25      30
Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
      35      40      45
Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
      50      55      60
Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
      65      70      75      80
Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr

```


<221> CDS
 <222> (67)...(1611)
 <223> mouse IMP dehydrogenase cDNA double mutant:
 Thr333Ile
 Ser351Tyr

<221> mutation
 <222> 1064
 <223> C to T mutation

<221> mutation
 <222> 1118
 <223> C to A mutation

<400> 31
 cctctgcggc gcggtcctcg gacggcgcg gttctcggag ccacgcgtct gtcttctctcc 60
 gtggtc atg gcg gac tac ctg att agc gga ggc acc tct tac gtg ccg 108
 Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro
 1 5 10

gac gac ggg ctc aca gcg cag cag ctc ttc aac tgc ggg gac ggc ctc 156
 Asp Asp Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu 30
 15 20 25

acc tac aat gat ttt ctc att ctt cct ggg tat atc gac ttc act gca 204
 Thr Tyr Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala 45
 35 40 45

gat cag gtg gac ttg acg tct gct cta act aag aag att aca cta aag 252
 Asp Gln Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys 60
 50 55 60

acc cca ttg gtt tcc tca ccc atg gac act gtc aca gag gct gga atg 300
 Thr Pro Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met 75
 65 70 75

gcc atc gcg atg gcg ctt aca gga ggt att ggt ttc atc cac cac aac 348
 Ala Ile Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn 90
 80 85 90

tgc aca cct gaa ttc cag gcc aat gaa gtt cgg aaa gtg aag aaa tac 396
 Cys Thr Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr 110
 95 100 105 110

gaa cag gga ttc atc act gac ccc gtg gtc ctt agc ccc aag gat cgt 444
 Glu Gln Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg 125
 115 120 125

gta cgc gat gtt ttt gag gcc aaa gcc agg cat ggc ttc tgt ggt atc 492
 Val Arg Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile 140
 130 135 140

ccc atc aca gat aca ggc cgg atg ggg agt cga ttg gtg ggc atc atc 540
 Pro Ile Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile 155
 145 150 155

tcc tca agg gac att gat ttc ctc aag gag gaa gag cat gac cgg ttc 588
 Ser Ser Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Arg Phe 170
 160 165 170

ttg gaa gag atc atg act aag agg gaa gat ttg gtg gtc gcc cct gcc 636
 Leu Glu Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Ala

175		180		185		190	
ggc gtc act ctg aaa gag gca aat gag att ctg cag cga agt aaa aag							684
Gly Val Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys							
		195		200		205	
gga aag ttg ccc att gtg aat gaa aat gat gag ctg gta gcc atc att							732
Gly Lys Leu Pro Ile Val Asn Glu Asn Asp Glu Leu Val Ala Ile Ile							
		210		215		220	
gcc cgg aca gac cta aag aag aat cgt gat tac ccc ctg gcc tcc aaa							780
Ala Arg Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys							
		225		230		235	
gat gcc aag aag caa ctg ctg tgt ggg gca gcc att ggc act cat gag							828
Asp Ala Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu							
		240		245		250	
gat gac aag tat agg ctg gac tta ctg gcc ctt gct ggt gtg gat gta							876
Asp Asp Lys Tyr Arg Leu Asp Leu Leu Ala Leu Ala Gly Val Asp Val							
		255		260		265	270
gtg gtt ttg gac tct tcc cag gga aac tcc atc ttc caa atc aat atg							924
Val Val Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met							
		275		280		285	
atc aaa tac atc aag gag aag tat ccc agt cta cag gtc att gga ggc							972
Ile Lys Tyr Ile Lys Glu Lys Tyr Pro Ser Leu Gln Val Ile Gly Gly							
		290		295		300	
aat gta gtc act gct gcg caa gcc aag aac ctc ata gat gca ggt gta							1020
Asn Val Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val							
		305		310		315	
gat gct ttg cga gtc ggc atg gga agt ggt tcc atc tgc atc atc cag							1068
Asp Ala Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Ile Gln							
		320		325		330	
gaa gtg ttg gcc tgt ggg cgg ccc caa gcc aca gca gtg tac aag gtc							1116
Glu Val Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val							
		335		340		345	350
tat gag tat gcc cgt cgc ttt ggt gtt cct gtt att gct gat gga gga							1164
Tyr Glu Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly							
		355		360		365	
atc caa aat gtg ggt cat att gcc aaa gct ttg gct ctt ggg gct tcc							1212
Ile Gln Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser							
		370		375		380	
aca gtc atg atg ggc tcc ctc ctg gct gcc acc act gag gcc cct ggc							1260
Thr Val Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly							
		385		390		395	
gag tac ttc ttc tca gat ggg atc cgg ctg aag aaa tac cga ggt atg							1308
Glu Tyr Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met							
		400		405		410	
ggt tct ctt gat gcc atg gac aaa cat ctc agc agc cag aac cga tac							1356
Gly Ser Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr							
		415		420		425	430

ttc agt gaa gct gac aaa atc aaa gtg gcc caa gga gtt tca ggg gca 1404
 Phe Ser Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala
 435 440 445

gtg cag gac aag ggg tct atc cac aag ttc gtt cct tac ctg att gct 1452
 Val Gln Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala
 450 455 460

ggc atc cag cat tcc tgt caa gac att ggt gcc aag agt tta acc caa 1500
 Gly Ile Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln
 465 470 475

gtc aga gcc atg acg tac tcg ggg gag ctt aaa ttt gag aag agg aca 1548
 Val Arg Ala Met Thr Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr
 480 485 490

tcc tct gct cag gtg gaa ggt ggc gtc cac agc ctc cat tcg tac gag 1596
 Ser Ser Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu
 495 500 505 510

aaa cgg ctt ttc tga aaacagatcc agtatatgcc ttgaattttt caataaaagt 1651
 Lys Arg Leu Phe *

ttgggaaaaaa aaaagtgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1707

<210> 32
 <211> 514
 <212> PRT
 <213> Mus musculus

<400> 32
 Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
 1 5 10 15
 Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
 20 25 30
 Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
 35 40 45
 Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
 50 55 60
 Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
 65 70 75 80
 Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
 85 90 95
 Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln
 100 105 110
 Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg
 115 120 125
 Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile
 130 135 140
 Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser
 145 150 155 160
 Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Arg Phe Leu Glu
 165 170 175
 Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Ala Gly Val
 180 185 190
 Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
 195 200 205
 Leu Pro Ile Val Asn Glu Asn Asp Glu Leu Val Ala Ile Ile Ala Arg
 210 215 220
 Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala
 225 230 235 240

Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp
 245 250 255
 Lys Tyr Arg Leu Asp Leu Leu Ala Leu Ala Gly Val Asp Val Val
 260 265 270
 Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys
 275 280 285
 Tyr Ile Lys Glu Lys Tyr Pro Ser Leu Gln Val Ile Gly Gly Asn Val
 290 295 300
 Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala
 305 310 315 320
 Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Ile Gln Glu Val
 325 330 335
 Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Tyr Glu
 340 345 350
 Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln
 355 360 365
 Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
 370 375 380
 Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
 385 390 395 400
 Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
 405 410 415
 Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser
 420 425 430
 Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln
 435 440 445
 Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile
 450 455 460
 Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg
 465 470 475 480
 Ala Met Thr Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser
 485 490 495
 Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg
 500 505 510
 Leu Phe

<210> 33
 <211> 5627
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Sequence of pMG
 plasmid from InvivoGen

<400> 33
 caccggcgaa ggaggcctag atctatcgat tgtacagcta gctcgacatg ataagataca 60
 ttgatgagtt tggacaaacc acaactagaa tgcagtga aaatgcttt atttgtgaaa 120
 tttgtgatgc tattgcttta tttgtgaaat ttgtgatgct attgctttat ttgtaaccat 180
 tataagctgc aataaacaag ttaacaacaa caattgcatt cattttatgt ttcaggttca 240
 gggggaggtg tgggaggttt tttaaagcaa gtaaaacctc tacaaatgtg gtagatccat 300
 ttaaattgta attaagaaca tgtgagcaaa agggccagcaa aaggccagga accgtaaaaa 360
 ggccgcggtt ctggcggttt tccataggct ccgccccctc gacgagcatc acaaaaaatcg 420
 acgctcaagt cagaggtggc gaaacccgac aggaactataa agataccagg cgtttcccc 480
 tggaagctcc ctctgctgct ctctgttctc gacctgccc cttaccggat acctgtccgc 540
 ctttctccct tcgggaagcg tggcgctttc tcatagctca cgctgtaggat atctcagttc 600
 ggtgtagggt gttcgctcca agctgggctg tgtgcacgaa ccccccgttc agccccaccg 660
 ctgcgcctta tccggtaact atcgtcttga gtccaacccg gtaagacacg acttatcgcc 720
 actggcagca gccactggta acaggattag cagagcgagg tatgtaggcg gtgctacaga 780
 gttcttgaag tgggtggccta actacggcta cactagaaga acagtatttg gtatctgcgc 840
 tctgctgaag ccagttacct tcggaaaaag agttggtagc tcttgatccg gcaaacaaac 900
 caccgctggg agcgggtggt tttttgtttg caagcagcag attacgcgca gaaaaaaagg 960
 atctcaagaa gatcctttga tcttttctac ggggtctgac gctcagtgga acgaaaactc 1020
 acgttaaggg attttggtca tggctagtta attaagctgc aataaacaat cattattttc 1080
 attggatctg tgtgttgggt ttttgtgtgg gcttggggga gggggaggcc agaatgactc 1140
 caagagctac aggaaggcag gtcagagacc ccactggaca aacagtggct ggactctgca 1200
 ccataacaca caatcaacag gggagtgcac tggatcgagc tagagtccgt tacataactt 1260
 acggtaaaatg gcccgctgg ctgaccgccc aacgaccccc gcccattgac gtcaataatg 1320
 acgtatgttc ccatagtaac gccaataggg actttccatt gacgtcaatg ggtggagtat 1380
 ttacggtaaa ctgcccactt ggcagtagat caagtgtatc atatgccaaag tacgccccct 1440
 attgacgtca atgacggtaa atggcccgc tggcattatg cccagtacat gaccttatgg 1500
 gactttccta ctggcagta catctacgta ttagtcacg ctattaccat ggtgatcgcg 1560
 ttttggcagt acatcaatgg gcgtggatag cggtttgact cacggggatt tccaagtctc 1620
 caccctattg acgtcaatgg gaggttgttt tggcaccaaa atcaacggga ctttccaaaa 1680
 tgtcgtaaac actccgcccc attgacgcaa atgggcggtg ggcgtgtacg gtgggaggtc 1740
 tatataagca gagctcggtt agtgaaccgt cagatcgctt ggagacgcca tccacgctgt 1800
 tttgacctcc atagaagaca ccgggaccga tccagcctcc gcggccggga acggtgcatt 1860
 ggaacgcgga ttccccgtgc caagagtgc gtaagtaccg cctatagagt ctataggccc 1920
 acccccttgg cttcttatgc atgctatact gtttttggct tggggtctat acacccccgc 1980
 ttctctatgt tataggtgat ggtatagctt agcctatagg tgtgggttat tgaccattat 2040
 tgaccactcc cctattgggt acgatacttt ccactactaa tccataacat ggctctttgc 2100
 cacaactctc tttattggct atatgccaat acactgtcct tcagagactg acacggactc 2160
 tgtattttta caggatgggg tctcatttat tatttacaaa ttcacatata caacaccacc 2220
 gtccccagtg cccgcagttt ttattaaaca taacgtggga tctccacgcg aatctcgggt 2280
 acgtgttccg gacatgggct cttctccggt agcggcggag cttctacatc cgagccctgc 2340
 tcccattgct ccagegactc atggctcgct gccagctcct tgctcctaac agtggaggcc 2400
 agacttaggc acagcacgat gcccaccacc accagtgtgc cgcacaaggc cgtggcggta 2460
 gggatgtgt ctgaaaatga gctcggggag cgggcttgca ccgctgacgc atttggaaga 2520
 cttaaggcag cggcagaaga agatgcaggc agctgagttg ttgtgttctg ataagagtca 2580
 gaggtaaact ccgttgcggg gctgttaacg gtggagggca gtgtagtctg agcagtactc 2640
 gttgtgcggc gcgcgccac cagacataat cagtgcagca ctaacagact gttcctttcc 2700
 atgggtcttt tctgcagtca cccgggggat ccttcgaacg tagctctaga ttgagtgcac 2760
 gttactggcc gaagccgctt ggaataaggc cgggtgtcgt ttgtctatat gttattttcc 2820
 accatattgc cgtcttttgg caatgtgagg gcccggaaac ctggccctgt cttcttgacg 2880
 agcattccta ggggtctttc ccctctcgcc aaaggaatgc aaggtctgtt gaatgtcgtg 2940
 aaggaagcag ttctcttggg agcttcttga agacaaacaa cgtctgtagc gacctttgc 3000
 aggcagcgga accccccacc tggcgacagg tgcctctgcg gccaaaagcc acgtgtataa 3060
 gatacacctg caaaggcggc acaaccccag tgccacgttg tgagttggat agttgtggaa 3120

```

agagtcaaat ggctctcctc aagcgtatct aacaaggggc tgaaggatgc ccagaaggta 3180
ccccattgta tgggatctga tctggggcct cgggtgcacat gcttttacatg tgttttagtcg 3240
agggttaaaaa aacgtctagg ccccccgaac cacggggagc gggttttcct ttgaaaaaca 3300
cgataatacc atgggtaagt gatattctact agttgtgacc ggcgcctagt gttgacaatt 3360
aatcatcggc atagtatatc ggcatagtat aatacgactc actataggag ggccaccatg 3420
tcgactacta accttcttct ctttcctaca gctgagatca ccggtaggag ggccatcatg 3480
aaaaagcctg aactcaccgc gacgtctgtc gcgaagtttc tgatcgaaaa gttcgacagc 3540
gtctccgacc tgatgcagct ctcgaggggc gaagaatctc gtgctttcag cttcgatgta 3600
ggagggcggtg gatatgtcct gcgggtaaat agctgcgcgc atgggtttcta caaagatcgt 3660
tatgtttatc ggcactttgc atcgcccgcg ctcccgattc cggagtgtct tgacattggg 3720
gaattcagcg agagcctgac ctattgcac tcccgcctg cacaggggtgt cacgttgcaa 3780
gacctgcctg aaaccgaact gccgctgttt ctgcaaccgc tcgcggagct catggatgcg 3840
atcgctgcgg ccgatcttag ccagacgagc ggggttcggcc cattcggacc gcaaggaatc 3900
gggtcaataca ctacatggcg tgatttcata tgcgcgattg ctgatcccca tgtgtatcac 3960
tggcaaactg tgatggacga caccgtcagt gcgtccgtcg cgcaggctct cgatgagctg 4020
atgctttggg ccgaggactg ccccgaagtc cggcacctcg tgcacgcgga tttcggctcc 4080
aacaatgtcc tgacggacaa tggccgcata acagcgggca ttgactggag cgaggcgatg 4140
ttcggggatt cccaatacga ggtcgccaac atcttcttct ggaggccgtg gttggcttgt 4200
atggagcagc agacgcgcta cttcgagcgg aggcacccgg agcttgcagg atcgcccgcg 4260
ctccgggcgt atatgtctcg catttgtctt cgatgcgacg caatcgtccg atccggagcc 4320
aatttcgatg ggcgtacaca aatcgccgc agaagcgcgg ccgtctggac cgatggctgt 4440
gtagaagtac tcgccgatag tggaaaccga cgcgccagca ctcgtccgag ggcaaaggaa 4500
tgagtcgaga attcgctaga gggccctatt ctatagtgtc acctaataatgc tagagctcgc 4560
tgatcagcct cgactgtgcc ttctagttag cagccatctg ttgtttgccc cctaataaaaa tgaggaaatt 4620
ccttccttga ccctggaagg tgccactccc actgtccttt cctaataaaaa tgaggaaatt 4680
gcacgcgatt gtctgagtag gtgtcattct attctggggg gtgggggtgg gcaggacagc 4740
aagggggagg attggaaga caatagcagg catgcgcagg gccaatttgc tcgagcggcc 4800
gcaataaaat atctttatct tcattacatc tgtgtgttgg ttttttgtgt gaatcgtaac 4860
taacatacgc tctccatcaa aacaaaacga aacaaaacaa actagcaaaa taggctgtcc 4920
ccagtgcagg tgcagggtgc agaacatttc tctatcgaag gatctgcgat cgctccgggtg 4980
cccgtcagtg ggcagagcgc acatcgccca cagtccccga gaagttgggg ggaggggtcg 5040
gcaattgaac cgggtgcctag agaaggtggc gcggggtaaa ctgggaaagt gatgtcgtgt 5100
actggctccg cctttttccc gaggttgggg gagaaccgta tataagtgc gtatgcgccg 5160
tgaacgttct ttttcgcaac gggtttgccg ccagaacaca gctgaagctt cgaggggctc 5220
gcactctctc ttcacgcgc ccgcgccta cctgaggccg ccacccacgc cggttgagtc 5280
gcgttctgcc gctcccgcc tgtggtgcct cctgaactgc gtccgcccgtc taggtaagtt 5340
taaagctcag gtgcagaccg ggcctttgtc cggcgctccc ttggagccta cctagactca 5400
gccggtctc cacgttttgc ctgaccctgc ttgtcact ctacgtcttt gtttcgtttt 5460
ctgttctgcg ccgttacaga tccaagctgt gaccggcgcc tacgtaagt atactacta 5520
gatttatcaa aaagagtgt gacttgtgag cgctcacaat tgatacttag attcatcgag 5580
agggacacgt cgactactaa ccttcttctc tttctacag ctgagat 5627

```

<211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Forward primer for amplification-based cloning of hIMPDH type II cDNA

<400> 34
 gctatctgca ggccgccacc atggccgact acctgattag 40

<210> 35
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Reverse primer for amplification-based cloning of hIMPDH type II cDNA

<400> 35
 catactcttc gccgaaaaga ctagatctcg atc 33

<210> 36
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Forward primer for T333I mutation of hIMPDH type II cDNA

<400> 36
 ggctccatct gcattatcca ggaagtgctg gc 32

<210> 37
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Reverse primer for T333I mutation of hIMPDH type II cDNA

<400> 37
 ccgaggtaga cgtaataggt ccttcacgac cg 32

<210> 38
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Forward primer for S351Y mutation of hIMPDH type II cDNA

<400> 38

cagcagtgtgta caaggtgtat gagtatgcac ggcgcttt

38

<210> 39

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Reverse primer for S351Y mutation of hIMPDH type II cDNA

<400> 39

gtcgtcacat gttccacata ctcatacgtg ccgcgaaac

39